

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCAATGGCGTCCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTC AAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTTGCA GTTGGCATT TGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG  
TCATTATTTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG  
ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCTTTGGAGTTGCTTGCTTCCA ACTGATTGGAATCTTTCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCTATTCTCTCT  
CTACCTTTAAGGACATTTAGGGTCCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTTACTGATAGACAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATT CATGTTAGATCG  
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

## FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
```

><subunit 1' of 1, 245 aa, 1 stop, 1 unknown

><MW: -1, pI: 8.36, NX(S/T): 1

MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLEKATNPVF  
 VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN  
 NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPSCKLEDCTPQ  
 RDADKVNNEGCFIKVMTIIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

# **FIGURE 3**

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT  
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT  
GTTCCCTCTTTCGGGGGTCCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT  
GCGGCTAACAGGGGCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG  
GGAATAAGCTCTGCAACTTTCTTTGGCATTTCAGTTGTTAAAAACAAATAGGATGCAAATTCC  
TCAACTCCAGGTTATGAAAACAGTACTTGGA AAACTGAAAACCTACCTAAATGATCGTCTTTG  
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG  
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC  
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT  
GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
GAAAAGTGTTCTGCCC GGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC  
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

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## **FIGURE 4**

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57



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## **FIGURE 5**

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTCAGCCCATTGCGC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTG  
CAAG**ATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTTCCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTC**TAG**CATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA  
AAAAAAAAAAAA

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## **FIGURE 6**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM  
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER  
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

### **Signal peptide:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 86-103, 60-75

### **Casein kinase II phosphorylation site.**

amino acids 82-86

### **Tyrosine kinase phosphorylation site.**

amino acids 144-151

### **N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

### **G-protein coupled receptors proteins.**

amino acids 44-85

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## FIGURE 7

AATTCAGATTTTAAGCCCATCTGTCAGTGGAATTTTCATGAACTAGCAAGAGGACACCATCTT  
 CTTGTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGGGAAAA**ATG**CTCTTTTGGGT  
 GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAATAAGATTGAAG  
 ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC  
 AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTAAGTGTGCTTCTGGATGTGACCGACCCAG  
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT  
 CTGATCAATAATGCTGGTGTTCCTGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA  
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC  
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTGCCTTGCA  
 ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAGGTTTCAATGACAGCTTAAG  
 ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA  
 ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA  
 GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAACTGAAAGGCAA  
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
 GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG  
 TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
 TCCCAAGGCAGT**GTGA**CTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT  
 TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA  
 TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG  
 CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT  
 ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG  
 ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTT  
 AAGTATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406

><subunit 1 of 1, 319 aa, 1 stop

><MW: 35227, pI: 8.97, NX(S/T): 3

MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT  
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW  
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF  
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEQYIEKSLD  
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK  
AELANPKAV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 136-152

#### **N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

#### **Glycosaminoglycan attachment site.**

amino acids 39-42

#### **N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

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## FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATG**GGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTTCCTGACGCCGCCAGTGGGCGGGGCCCTTGGGCGGTCGCCACCACT  
 GTAGTCATGTACCCACCGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG  
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGGCGGCTCGTGCTGGAGGAAATGGA  
 AGCAACTGTGAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT  
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAAACCAGCAAATCCACCCGCTTACCAG  
 CTCCTCAGAAGGCGGACACCGACCCCTGAGAACTTACCTGAGATTTTCGTACAGAAGACACAA  
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAAGCCCCTGTGGATCCCCGCCCGGAAGGAG  
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG  
 CTCCCTTCAAGAAGAGCAGAAAGTGCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG  
 CACACCAGTGCATCTGAACATCGCCAGAAGGGCGTGATTGACGTCTTCTGTCATGCATGGA  
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT  
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT  
 GAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGAAGAAGTTACACTTTGAAAAGGACG  
 TGGACGTCAACCTGTTTGAAGACACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC  
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC  
 CTTCAGAACACCATCCAAGATTCCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC  
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTACAGCTGGAGTTCCGG  
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA  
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATAACCCACAGTG  
 GCCTCTTACCCACCTGGGCGTATTCACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
 AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACTCCGAGCCCAGTAAGCTCACCTTTG  
 TGGGGGAGCTTGCCACGGCCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCA  
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCCAGGA  
 GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG  
 TGCACTTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG  
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGGA  
 CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTCACACGGGTCC  
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCCGAGCCTAGGGAC  
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCACCCCTCTGCCTATCT  
 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG  
 CTGGGTCTGTGGCATTTCCTCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCCAGGCT  
 CTGAACTGGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA  
 GGCCGTCAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCTGCTTCTC  
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA  
 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGTGCAGC  
 TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGTCTGGAGGGGCTGCCGTGA  
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC  
 CTGGCCGCCCCGCAGGGGGCTTGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCCCT  
 CCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAA

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## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDN  
 SKSWRRRSCWRKWKQLSRLQRMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE  
 IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGQTQEEAT  
 KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSSRAEVPTKPPLPPARTQGTPVHLNY  
 RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA  
 RKWVSKKLHFEKDVDVNLFFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI  
 PYSDVNIGTGVAHPPRWTSdstVAEVTSIQLEFRELsRLTGDKKFQEAVEKVTQHIHGLSGK  
 KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT  
 HLLRHSEPSKLTFVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ  
 MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLRPETVESLFYLYRVTGDRKYQDWG  
 WEILQSFSRFTRVPSSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD  
 AYVFNTAHPLPIWTPA

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

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## FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
CGCCTCTCCGCACG**ATG**TTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCGTCTTCCACCTGTTTCGTGGC  
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG  
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT  
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA  
GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC  
CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
CCTTCCACGTGGCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC  
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC  
GCCCTCGGGAATCACAACCTGGGTACAAGACATTTGCCCACCTGCATGACCCAGCCTGGCGG  
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGGCC  
CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  
AGCT**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
CAAGGCCTCAGGTTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTCTGTCCG  
GGACCCCCCCTGCCTTCCTGCTCACCCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG  
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCTACTCTGACCTCCTTCACGTGCCC  
AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310



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## **FIGURE 13**

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC  
CCTGTTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGT  
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 14**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ  
PRGEGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

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## FIGURE 15

GGGACCCATGCGGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG  
GAGCATGTCCGCGCCGGGAAGGCCCGTCCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG  
GCCCCGCGCCGCGCTCCTGCCCGCCGGGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCG  
CTCGCCCCGCGAGGCCCGGCCCGCAGC**ATG**GAGCCACCCGGACGCCGGCGGGGCCGCGCGCA  
GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGGCGCG  
GCGGCGGCGCCGCGGGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGC  
AGGGCGGCGGGCGCCGCCGAGGGCAAGGTGGTGTGAGCAGCCTGGAACCTCGCGCAGGTCCT  
GCCCCCAGATACTCTGCCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCG  
AGCTGAAGAATGGCTCATTTTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT  
CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCATCTCTAAAAAGATTGGATCT  
GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCGAGGACTCACCAATCTGGTTC  
GGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTTGATTATCTTGCG  
TCATTACGGTCTTTGGAATTCCAGACTGAGTATCTTTTGTGTGACTGTAAACATACTGTGGAT  
GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT  
CACTGCAGGCCCAACCAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT  
GAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACAGCCT  
TCCTTTCCAGTGATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAGGATG  
GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAACATGATTCACAAC  
TGCTCCTTGATTGCAAGTGCCCTAACCATTCTAATATTCAGGCTGGATCTACTGGAAATTG  
GGGCTGTCATGTCCAGACCAAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG  
AGAGTTCTGCACAGTACTGTCCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG  
CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG  
GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT  
TTTGGGCAGATGATGATTATTCTCGCTGTCAGTATGCAAATGATGTCACTAGAGTTCTTTAT  
ATGTTTAAATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC  
TTACACTGTGGAAGCAGCCAACTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA  
TTGAAAAATTTTGAAGATTTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT  
GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCCTGTGGCTGGCGCAGAGGGAAGC  
TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG  
GAGCTCACGTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT  
ACTGGCTTCACGGGGATGACCTGTACCGTGTTCAGAAAAGTGGCAGCCTCTGATCGTACAGG  
ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT  
GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT  
AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA  
AAAGATTTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAATA  
ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTTGCTTTTGATTCCCTTT  
CTTCACATAAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAAATACT  
ATTGTTACATGTGAAAAAATTTTATTGACTTAAAAGTTTATTTATTTGTTTTTTTGCTCCT  
GATTTTAAAGACAATAAGATGTTTTTCATGGGCCCTAAAAGTATCATGAGCCTTTGGCACTGC  
GCCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACCAGGTGTTTAAATCAAGCAAGCTGTAT  
ATCAAAATTTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTTTAAAAAAGTATTTCA  
TTGAAGCAAGCAAAATGAAAGCATTTTTTACTGATTTTTTAAATTTGGTGCTTTAGATATATTT  
GACTACACTGTATTGAAGCAATAGAGGAGGCACAACTCCAGCACCTAATGGAACCACATT  
TTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAAATCTCACAG  
TACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCCAGTCATTTTAAATGGC  
TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAATA  
TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

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## **FIGURE 16**

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
VVCSSLELAQVLPPDTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT  
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPLELPSFYMTP  
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT  
ISNIQAGSTGNWGCCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGD FRWPRTLGIT  
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL  
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA  
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT  
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
384-390, 403-409, 554-560

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## **FIGURE 17**

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTCGGA AAAAAGAAAACATTTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAA  
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA  
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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## **FIGURE 18**

MSRSSKVVGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

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## FIGURE 19

CTGTCGTCTTTGCTTCAGCCGCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC  
CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC  
GCTGCCATGCCAGTGACGGTAACCCGCGACCACCATCACAACCACCACGACGTCATCTTCGGG  
CCTGGGGTCCCCCATGATCGTGGGGTCCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC  
CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC  
GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGGTCTCTGCTTCTCCGTGACCCTGATCA  
TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC  
ATCACCTTCGCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC  
CTATGTCCAGTTCCTGTCCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT  
CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGGCCCGGGCCGGCGAG  
ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG  
CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG  
GAGTGCACCAACGTGCTACCCATCCCCTTCCCCAGCTTCCTGTGCGGGCTGGCCTTGCTGTC  
TGTCTCTCTATGCCACCGCCCTTGTTCTCTGGCCCCCTTACCAGTTCGATGAGAAGTATG  
GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT  
GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC  
TGACCTGGTGCACCTCTGCCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC  
CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
TCCGCCTTTCCTCTGTTTTCTCTTCTGTCTCCCCTCCCTCCACCTTTTTCTTTCTTCC  
CAATTCCTTGCACTCTAACCAGTTCCTGGATGCATCTTCTTCCCTTCCCTTTCCTCTTGCTGT  
TTCCTTCCCTGTGTTGTTTTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTTTTTT  
CTTTTCTTTCTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCCAGGCTGGAG  
TGAGTGGTGCATCTCAGCTCACTGCAACCCCCGCTCCTGGGTTCAGCGATTCTCCTCC  
CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT  
TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGCTGCTGCGCTTCTTATCTGCCTGT  
TTTGCAAGCACCTTCTCCTGTGTCCTTGGGAGCCCTGAGACTTCTTTCTCTCCTTGCCTCCA  
CCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGCAGCCGTCCATGCCACAGCCCC  
CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC  
GTGTGTGTGTGTGTGTGTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT  
CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCCTTTAAATTAAAAACATATATATATATAT  
ATTTGGAGGTGAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG  
CCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC  
CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT  
CTGTGGTATGAAAAAG

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## **FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG  
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY  
VQFLSHGRSRDHAI AATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI  
IFAFISDPNLYQHQP ALEWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV  
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD  
LVHSAHLVFVKV

### **Important features:**

#### **Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

#### **N-glycosylation site.**

amino acids 66-69

#### **Glycosaminoglycan attachment site.**

amino acids 18-21



[illegible]

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## **FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSSHVKVHMDPNYCHPSTSLHLCS  
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY  
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDITLCSLCSLEDGLLGSPARLASQLLGDE  
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER  
QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

## FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCT  
GGCACCTCCTGCTCAGTGCGACATTGTCACTTAACCCATCTGTTTTCTCTAATGCACGA  
CAGATTCCTTTCAGACAGGACAACCTGTGATATTTAGTTCTGATTGTAAATACCTCCTAAG  
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA  
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG  
AAGCCTACAATGTTGGCCTTAGCCAAAATCTGTTGATTTCAACGTTGTTTTATTCACTTCT  
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAAGTTT  
TTAAAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAACTCAGATAAA  
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTTGAATCTACCCAACAA  
CAGCCACGGAATAACAGATTTCTCCAGTAACCTCATCAGCAGAGCATTCTTTGGGCAGTCTAA  
AACCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT  
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCGATA  
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG  
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA  
TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTACCAATAATTCAAACTCTTTCCAA  
ATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT  
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAAAAGGAAAAC  
GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA  
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAAT  
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCCTATGGATGACATACC  
TCCACTTCGTACTTCTGTATTAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA  
CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT  
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
CCAAAGGTTTTCTTTCTTACAATTTTTTGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT  
TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT  
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCACCAAAAAATTCTAAA  
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG  
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC  
TAGTACGTTATAATTTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA  
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT  
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA  
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

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## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKT MENKPISLESEANLNSDKENI  
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA  
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE  
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL  
GVSLTLVGYLLCGKRKTDSEFSHRRLYDDRNEPVLRLDNAPEPYDVSGNSSYYNPTLNSA  
MPESEENARDGIPMDDIPPLRTSV

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domain:**

amino acids 235-262

### **N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311

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## FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
AGCCCCGAAGATTCACT**ATG**GTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG  
AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
CTTAGGCCTTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTTGATTCTGAGGATCCTGCA  
AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA  
GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAG  
CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAACCTGC  
TATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG  
CAAACCTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG  
TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA  
AAGTCCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA  
ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**  
**AA**GAGGCAACAGATAGAGTGTCTTGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
CATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT  
AAAAAAAGGAAAAAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAA  
TGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTTTCTTTGCATTTATAG  
GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC  
GTTGTTTTTTTTGTTTGTGTTTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG  
GTGGAGCAATTTTAAATTTGAAATATTTTAAATTGTTTTTGAACTTTTTGTGTAAAATATA  
TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCATTTTGTACAACTTTCTGAATTTAGA  
AATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT  
TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG  
AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA  
CCCTATAATAAATTTTACTCTATACAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF  
 ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA  
 IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG  
 RYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNRKSFRLRRRDLLLGFNKRAIDKCWKIR  
 HFPNEFIVETKICQE

### **Type II transmembrane domain:**

amino acids 53-75

### **N-glycosylation site.**

amino acids 166-170

### **Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

### **N-myristoylation site.**

amino acids 66-72, 103-109

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

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## FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT  
CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTTCGGCGGGAGACCCAGTCCTGTACGCC  
AAGGAACTGGTCCTGGGGGCACCATGGTTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG  
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCCTGAAGGCCACGTT  
CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCCTGGGG  
GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA  
TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC  
GTGGACCAGAGTGACCGGGCCGGGGGCCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
CGACAGCAGGCCCGAGGAAGCCCTGGATTTCCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG  
CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG  
GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA  
GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG  
AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCCAG  
GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGCCCCCTGTGCTTGCAGCAGTGTCCACCCAG  
TGTCTAAACAGTCCTCCCGGGCTGCCAGCCCTGACTGTGCGGGCCCCCAAGTGGTCACCTCCCC  
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG  
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA  
GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC  
ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC  
CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTTTAAACA  
GCTACAGGGTAAATCCTGCAGCACCCTCTGGAAAATACTGCTCTTAATTTTCTCTGAAGG  
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAATCCTC  
TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG  
GATCAGGTTGAATGAATGGAACCTTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
GCTGTGTTTGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG  
CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTGTGCTCACACATTGTCTGGCAGCCTG  
TGTCCACAATATTCGTCAGTCCTCGACAGGGAGCCTGGGCTCCGTCCTGCTTTAGGGAGGCT  
CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT  
CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAAAAA  
AAGA

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## **FIGURE 28**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV
```

### **Signal peptide:**

amino acids 1-25

### **Transmembrane domain:**

amino acids 94-118

### **N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248



[illegible]

amino acids 301-304

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**FIGURE 31**

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCCGGGGCGGTGCTCACCG  
 TGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGACATCTTCA  
 CTCTCCTGCTGCGCTGCACCGGAGCTTGGTGTGTGCGAGGAGAGTGAGGGGAAG**ATGT**GTTTCTGAACAAGC  
 TGCTGCTACTTGCTGTCTGGGCTGGCTTTTCCAGATTCCCACAGTCCCTGAGGACTTGTTCTTTCTGGAAGAGG  
 GTCCCTCATATGCCCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCTGTGGTGGACCAGC  
 AGCTGCTCTACACCTGCTGCCCCACATCGGAGAGCTCCGGAACCTGCTCGCTTCGTGGGTGTCAGGCAGTAGTG  
 GACGGAGTGGGGGCTTCATGAGGAAAATCACCCCCACCACTACCACCAGCCTGGGAGCCCCAGCCTTCCAGACCA  
 GCCAGGGGCTGCAGGCACAGCTCGCCCAGGCCTTTTTCCACAACCAGCCGCCCTCCTTGCGCCGGACCGTAGAGT  
 TCGTGGCAGAAAGAATTGGATCAAACCTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGGCCAGG  
 CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCCAGCCAGCTGTTGGAGATCT  
 TGTGTTCCAGCTGTGCCCTCACGGGGCCCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG  
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC  
 TTGCAACAGAGAAAGCCTGTGCTTGGCTGTCAGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG  
 TGAGTCGCACACTTCGAGCCCAGGCTCCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCC**TGAC**  
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCCCTGACGAGGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC  
 CAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG  
 GAGTTAGCTTCCCTCCTCGTTGCAGATCAAATTCCTATCCTAGGGCCCCCGGCACAGTACAGGCTGGAGAGAGGG  
 CAGGCTCGAAGGCTTCTGCACATGCTGCTTCCCTTGTGGAAGGAAGACTTTCAGGGGCGGTTCCGCTGCAGCTG  
 CTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGCTGCTATTCTTGCTA  
 CGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCCTGCCTGGGCAGCCTCCACCAGGCCAG  
 TGGCCAGGGGACTTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCCACCTGCCAGAACCC  
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC  
 CTGCCTTGGGCATTGCACCAGAACCCTGGACCCCGCCTCACGAGGAGGCCCAAGTGCCCAATGCAGACCCCTCAC  
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCCTGCTCTAAGGGTGTCACTGCCTGGCATCCCAACCGCA  
 ATCCTAGAGGAAGGAGAGTTGGCCTGATTTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCTGGAGTAGAA  
 GAGGTGGTGTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTGGGCTTGTCAACACAGAATTCAAGCCT  
 CATTTGCTATCCCAGCATCTCTTAAACTTTGTAGTCTTGGAATTCATGACAGAGGCAAATGACTCCTGCTTAAC  
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT  
 ATAAATGCCTAACACAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCCTGAGGTGGCG  
 GACTGCCTGAGGTGAGGAATTCAAGACCAGCCTGGCCAACATGGCAAAACCCCATCTCTACTAAAAATAAAAAA  
 TTATTAGCTGGGCATGGTGGTGTGTGCTGTAATCCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC  
 CTGGAGGTGGAGGTGTCAGTGAGCCGAGGTGCGACCACTGCACTCCAGTCTGGGTAACAGAGCGAGACTTTCTAG  
 AAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCTTGTACCTTACAGCCCTG  
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTTAGAGCTTTTATAGATAAA  
 CTGGTTTTCTTTAAAAAAGGGCTTTTATTAATAATCTCCCCACACGATGGCTCCTGCAATCTGCCACAGCTC  
 TGGGGCGTGTCTGTAGGGAAAGGCCCTGTTTTCCCTGAGGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG  
 GCCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTGCCGGGCACAGAGCTGCGGGGTCTGGGGGACCGGG  
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGTCTCTTAACCGACACCCTGAGGTGCTCCTGAGATGCTG  
 GGTCCACCCTGAGTGGCACGGGGAGCAGCTGTGGCCGGTGCTCCTTCYTAGGCCAGTCTGGGGAACTAAGCTC  
 GGGCCCTTCTTTGCAAAGACCGAGGATGGGGTGGGTGTGGGGGACTCATGGGAATGGCCTGAGGAGCTACGTGT  
 GAAGAGGGCGCCGGTTTGTGGCTGCAGCGGCCTGGAGCGCCTCTCTCCTGAGCCTCAGTTTCCCTTTCCGTCTA  
 ATGAAGAACATGCCGTCTCGGTGTCTCAGGGCTATTAGGACTGCCCTCAGGAAGTGGCCTTGGACGAGCGTCAT  
 GTTATTTTCACAACTGCTCTGCGACGTTGGCCTGGGCACGTATGGAATGGCCATGTCCCTCTGCTGCGTGGAC  
 GTCGCGGTGCGGAGTGCGCAGCCAGAGGCGGGGCCAGACGTGCGCCTGGGGGTGAGGGGAGGCGCCCCGGGAGGG  
 CCTCACAGGAAGTTGGGCTCCCGCACCAACAGGCAGGGCGGGCTCCCGCCCGCCGCCGCCACCACCGTCCAGG  
 GGCCGGTAGACAAAGTGGAAGTCGCGCTTGGGCTCGCTGCGCAGCAGGTAGCCCTTGATGCAGTGCGGCAGCGCG  
 TCGTCCGCCAGCTGGAAGCAGCGCCCGTCCACCAGCACGAACAGCCGGTGCAGCT

amino acids 278-282

## FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTTCTGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG  
AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC  
TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG  
AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT  
CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA  
GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
AACAAAGACACTGCCCTCTCGGTGCCACCAAGTGTGATTGTGAGCAGCTCCAGCCACCTGCT  
GGGCACCAAGCTGGGGCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC  
CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCTGGGCCATTCC  
AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT  
CATCTTCTGGGGGCCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC  
AGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGG  
CAATTTGACGACCTCTTCCGGGGTGAGACGGGGCAAGGACAGGGAGAAGTCTCATTCTGTGTT  
GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG  
GCATGGTCCCCCCCCAACTACTGCAGCCAGCGGGCCCCGCCTCCAGCGCATGCCCTACCACTAC  
TACGAGCCCCAAGGGGCCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG  
CAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGGCCAGCTGTATGGCA  
TCACCTTCTCCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG  
AGGAGAAGCAGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG  
CTGGAGTGTCTCCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC  
TGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC  
TTGTGACAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTTCTGAGTCAATCTG  
AGGCTAAGGACATGTCTTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCCA  
ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACTTGGTGTG  
CCCCCTCAATTTCCAGCACCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC  
GGCCAGAGAATTTGTGGGGTTGTGGAGGTTGTGGGGGCGGTGGGGAGGTCCAGAGGTGGGA  
GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCTTCCCCCTCTCTGGG  
CACCTTCTGCCCACACCAAGTTTCCAGTGCGGAGTCTGAGACCCTTTCCACCTCCCCTACAA  
GTGCCCTCGGGTCTGTCTTCCCCGTCTGGACCTCCCAGCCACTATCCCTTGCTGGAAGGCT  
CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTAGGGTATTTTTTGC  
GCAAACCTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT  
TAGCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCT  
CTAGCAGGGAGGTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGCCCCCTTGTCTGGAGTCA  
CTGGGGGCTTCCGAGGGTCTCCCTCGACCCTCTGTCTGCTGGGATGGCTGTGCGGGAGCTGT  
ATCACCTGGGTTCTGTCCCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGG  
GGTGTGTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA  
GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG  
GGCGGTGACTGCCCCAGACTTGGTTTTGTAATGATTGTACAGGAATAAACACACCTACGC  
TCCGGAAA

## **FIGURE 34**

MSSNKEQRSVAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
GNKTLPSRCHQCIVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH  
SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQKPQGS LVRVIQRAGLVFPNMEAYAVSPGRM  
RQFDDLFRGETGKDREKSHSWLSTGWFTMVI AVELCDHVHVYGMVPPNYCSQRPRLQRMPIYH  
YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

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## FIGURE 35

GTTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT  
 GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCTGG  
 GGCAAAGGTGAAAGAGTTTTCAGAACAAAGCTTCTTGGAAACCCATGACCCATGAAGTCTTGTGACATTTATACCGT  
 CTGAGGGTAGCAGCTCGAAACTAGAGAAGTGGAGTGTGGCCAGGGACGGCAGTATCTCTTTGTGTGACCCCTGGC  
 GGCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG  
 AGGCCTGAGGTACACTGGCTTGCCTCCTCTAGCCACAGCAGGCTGCTTTGCTGACTTGAACGAGGTCCCTCAG  
 GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACTCCCA  
 AGGATGAATGTAACCTGGCGCTGAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCACC  
 CACGGGACCTCGTCATCACTGCCCTTAACAACCACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCCTGCG  
 GGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG  
 ATTGAAGTGGATGAGGGAAACACAGCAGTCATTGCCTGCCACCTGCCTGAGAGCCACCCCAAAGCCAGGTCCGG  
 TACAGCGTCAAACAAGAGTGGCTGGAGGCTCCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT  
 GTGAATGCCAGCAGGAGGACGAGGGCATGTACAAGTGTGACGCTACAACCCAGTGACCCAGGAAGTGAAAACC  
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCCAGAGGCC  
 CAAACCATCATCGTCACCAAAGGCCAGAGTCTCATTTCTGGAGTGTGTGGCCAGTGGAAATCCACCCCCCAGGGTC  
 ACCTGGGCCAAGGATGGGTCCAGTGTACCCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTCCTCATCGAC  
 ACCACAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAATGGGGTTGGGCAGCCGGGGCAGCGGT  
 ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGGTCATCCCTGGGGC  
 CAGAGTGCCAAGCTTACCTGTGAGGTGCGTGGGAACCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCCC  
 CTCATCTCCAGCCAGCGCTCCGGCTCTCCCGCAGGGCTTCCGCGTGTGCTGAGCATGGGGCTGAGGACGAAGGC  
 GTCTACCAAGTGCATGGCCGAGAACGAGGTTGGGAGCGCCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC  
 ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATCACCTCCAAACTCGGCAAC  
 CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCCAGACCCCAACGTAGTGGGGCTGCTTCCCCGAAGTGT  
 CCAGGAGAGAAGGGGCGAGGGGCTCCCGCCGAGGCTCCCATCATCTCAGCTCGCCCCGACCTCCAAGACAGAC  
 TCATATGAAGTGGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTACTATGTGGTGAAACAC  
 CGCAAGCAGGTACAAATTCCTCTGACGATTGGACCATCTCTGGCATTCCAGCCAACAGCACCCTGACCCCTC  
 ACCAGCTTGACCCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAAGTGTGCGGGAGAGGGCCAGACAGCC  
 ATGGTCACCTTCCGAAGTGGACGGCGGCCCAAACCCGAGATCATGGCCAGCAAGAGCAGAGATCCAGAGAGAC  
 GACCCTGGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACCAGCGCCGCTCTCCCCCCCAGAAGCTCCCGACAGG  
 CCCACCATCTCCACGGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTTCCTCAATC  
 CAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCAGCGCCCTCCCCCA  
 TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG  
 CTGGGGGAGAGCGAGGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGCGGGCTACAGCGGTGCGGTGTACGAGAGG  
 CCCGTGGCAGGTCTTATATCACCTTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC  
 CCAGCAAGTAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTGAACATGATAGT  
 GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCCTAC  
 GACATTAAGATGCAGTGTCTCAATGAAGGAGGGGAGAGCGAGTTAGCAACGTGATGATCTGTGAGACCAAGCT  
 CGGAAGTCTTCTGGCCAGCCTGGTGCAGTGCACCCCCAAGTCTGGCCCCACCACAGCCGCCCCCTTCTGAAACC  
 ATAGAGCGGCGGTTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGGTGCTC  
 CTGGGCTCCATCGTTCTCATCATCGTCACCTTCATCCCTTCTGCTTGTGGAGGGCTGGTCTAAGCAAAAACAT  
 ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCCACCCTCTGCCCCGTATACTATGGTGCCATTGGGAGGACTC  
 CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG  
 AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGGCTGAAGCCCCAGCAGCACTGCCAGGCGAGCTTCAG  
 CAGCAGAGTGACACCAGCAGCCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCCAAAGTCACCAGATC  
 ACGAGGGGTCCCAAGTCTAGCCCGGACGAGGGCTCTTCTTATACACTGCCCGACGACTCCACTCACCAGCTG  
 CTGCAGCCCCATCAGCACTGCTGCCAACGCCAGGACGACCTGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC  
 CCGACAGTCTGTCTGGAAGCAGTGTGGGACCTCCATTTCACTCAGGGCCCCCATGCTGCTTGGGCCTTGTG  
 CCAGTTGAAGAGGTGGACAGTCTGACTCTGCCAAGTGAAGTGGAGGAGACTGGTGTCCCCAGCACCCTGAGG  
 GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCCGGGGCCACTGGTGGTGTGTCTTTTGAACACCACT  
 CTCACAATTAGGCAGAAGCTGATATCCAGAAAGACTATATATTTGTTTTTTTTTAAAAAAGAGAAAAA  
 AGAGACAGAGAAAATTGGTATTTATTTTCTATTATAGCCATATTTATATATTTATGCACTTGTAAATAAATGTA  
 TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTTACCCGTTGAGGTTGGAGAGGGAAAAATAAGAAGCTGCCA  
 CCTAACAGGAGTCACCCAGGAAAGCACCGCACAGGCTGGCGCGGGACAGACTCCTAACCTGGGGCTCTGCAGTG  
 GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTTCATCAGGACA  
 TGAGGGAACAGCAAGGGGACGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGTACGGGAA  
 ACATTTTCTAAGATGCCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAACCACTTCCAGAAT  
 CAATAATCCGTGGCAACATATCTCTGTAAAAACAAACACTGTAACCTCTAAATAAATGTTTAGTCTTCCCTGTAAAA

amino acids 16-30 (type II), 854-879



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## FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC  
CCAGGCTCCCGCGGCCGACCCCCGCGCAAC**ATG**CAGCCCACGGGCCGCGAGGGTTCCCGCGC  
GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC  
AGCCTCTTCACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
CACCCCCAAAACCTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACCTCG  
TGGACGGCCACAATGACCTGCCCCAGGTCTTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
GTTAACCTGCGAAATTTTCAGCCATGGTCAGACCAGCCTGGACAGGCCTTAGAGACGGCCTCGT  
GGGTGCCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCCTCCTACTCTGAACCTCGAGCTT  
GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG  
TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT  
ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACAC  
CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTTG  
AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG  
TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT  
GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAAATTATGACGGGACT  
GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT  
GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT  
TCAGACAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT  
CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC  
TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCT  
CCCCATACCTTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC  
TGCT**TGA**CACAGTCGGTCCCCGCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

## **FIGURE 38**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS  
 ALTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSGHQ  
 TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS  
 QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT  
 SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL  
 LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV  
 STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYGQLSTSCH  
 SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-36

#### **Transmembrane domain:**

amino acids 313-331

#### **N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

#### **N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

# **FIGURE 39**

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**  
AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAA  
GAGTTCTGAAGATATCCGGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
ACATGGCCTTCCTGATGCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC  
AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG  
TGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG  
CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCTCCTT  
CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT  
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA  
ATGGAGACATTTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG  
CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCTTGGAAGATAAAGCTGGGTCTTCA  
GGAATCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTACAGCATGTGTTCTTTCTGCAGTG  
GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACCTGGA  
AGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT  
CTGCTGCCGGTCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC  
CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGAATCTGAA  
CACCACAGCCCCTGTACTTGGGTGCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGA  
GAGAAAATTTGTCCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTG  
TTTTATTTCTCTCA

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## **FIGURE 40**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM  
PVPGH DVEAYCLLCECRYEERSTTTIKV IIV IYLSVVGALLLYMAFLMLVDPLIRKPDAYTE  
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 90-112

#### **N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50

# FIGURE 41

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTTCATAGGGTCTGGGTCCCCGA  
 ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGGACCCAAGTGAGGGGGCCCCGTGTTGGGGTCTCCC  
 TCCCTTTGCATTCCCAACCCCTCCGGGCTTTGCGTCTTCTGAGGGACCCCTCGCCGGGAGATGCGCGCTTGATG  
 CGGAGCAAGGATTTCGTCTGCTGCTGCTCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT  
 TCGCGGGCCAACTCAACTCCATCAAGTCCCTCTCTGGGCGGGGAGACGCCTGGTCAAGCCGCAATCGATCTGCG  
 GGCATGTACCAAGGACTGGCATTCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCCTACCCTTGTAGCAGT  
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA  
 AAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT  
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC  
 TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAAGGCATGAAGGA  
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAAATCTGCAAA  
 CCAGTGTCTCCATCAGGGGGAAGTCTGTACCAACAACGCAAGAAGGGTTCTCATGGGCTGGAAAATTTTCCAGCGT  
 TGGGACTGTGCGAAGGGCCTGTCTGCAAAAGTATGGAAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG  
 TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG  
 CATGGTGGAAAATAAGGTTTCAAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACA  
 AAAGGGAGAAAAGAAAACATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG  
 CAACTTGTCTATGTAAATAATGTACACATTTGTGGAAAATGCTATTATTAAAGAGAACAAGCACACAGTGGAAAT  
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTGGTGTGCTGGAGGAGAGGTTTCTTTCAGATTGCTGATTGC  
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAATACTCCTAGAATAACTTGTTA  
 TACAATAGGTTCTAAAAATAAAATGCTAAACAAGAAATGAAACATGGAGCATTGTTAATTTACAACAGAAAAT  
 TACCTTTTGATTTGTAACACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT  
 TTCCAAATAAATTGCAAAATAATGGCCAGTTGTTAGGAAGGCCCTTTAGGAAGACAAATAAATAACAAACAAACAG  
 CCACAAATACTTTTTTTTTTCAAATTTTAGTTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAAACAGTTCC  
 TTCAGATTCTACGGAATGACAGTATATCTCTCTTATCCTATGTGATTCTGCTCTGAATGCATTATATTTTCCA  
 AACTATACCCATAAATTGTGACTAGTAAATACTTACACAGAGCAGAATTTTCACAGATGGCAAAAAAATTTAAA  
 GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT  
 GATAGAATTAGATTGGTAAATACATGTATTACATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG  
 CACTGGAGTAAGCAAGAAAATTGGGAAAACCTTTTCGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG  
 AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT  
 CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCCGTACTATCCTCAAATTATTTATTTTATAG  
 TGCTGAGATCCTCAAATAATCTCAATTCAGGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG  
 TTTTATTGCCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAAACCTCTGCAGCATCTG  
 CTTTATTGCCAAAGGGCTAGTTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTA  
 ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATCTTTGAAACCACTTTACTACTTTTTTTAACTT  
 AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAACTTTTG  
 TAGACCACAATTCACTTTTTGTGTTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG  
 AGATTGAGTTTGAGCCTGTATATCTATTAATAAATTTCAACTTCCACATATATTTACTAAGATGATTAAGACTTA  
 CATTTTCTGCACAGGTCTGCAAAAACAAAAATTATAAACTAGTCCATCCAAGAACCAGGTTTGTATAAACAGGT  
 TGCTATAAGCTTGTGAATGAAATGGAACATTTCAATCAAACATTTTCTATATAACAATTATTATATTTACAAT  
 TTGGTTTCTGCAATATTTTTCTTATGTCCACCCCTTTAAAAATTTATTTTGAAGTAATTTATTTACAGGAAATG  
 TTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC  
 TTTGTAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTTCTCCTCTAAAAACTGAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 42**

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRC  
NN  
GICIPVTESILT<sup>1</sup>PHIPALDGTRHRDRNHGHYSNHD<sup>2</sup>LGWQNLGRPHTKMSHIKGHEGDPCLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQ<sup>3</sup>RKKGSHGLEIFQ<sup>4</sup>RCDCAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

## FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAA  
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT  
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTTAACATACTTGTGAAAATACTTG  
ATGTGTTTTTAAAGCCTTGGGCAGAAATTCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT  
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA  
 TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
 CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACCTACTACTTCTTGGGACCTCAAGCC  
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCCCTCCT  
 CCTGGTTTGGAGTCCTTTCCCTTCCCAGGCAAAACCTTCGAGAATCAACACCTGGAGACAGTCC  
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAATATCTCTGTGTCTG  
 TCCACCAGCCACAGCCCCAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG  
 ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT  
 TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG  
 AAAATAGTAATCAGATTCCCATCAGCTTGTATTGGAAGTCTTTAAGTGAGCCTTTGAATACA  
 TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTTCCGTCATTACCTCCTG  
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCCCTCTTATGACC  
 AGAGTTCTGTGCATAACAGGATCCCATAACAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA  
 GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAAAACAGAGGAAGAGGATAGCTCACGTGA  
 TGTGGAAAACACCAGTTGGTCAATGGCTCATTCGTTAAAAAGCAGCCCTTTTGCTTTTTTGT  
 TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT  
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCATAAATCCCAGTGCTTTGGGGGGCC  
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAAACTC  
 TGTCTCTACTAAAATACGAAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCAG  
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
 GTCTGAAAAGA

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## **FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
PSTQQNSTSHPTTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP  
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPQPKHIKLAKRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPTYQSPVSSSESAP  
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

**Signal peptide:**

amino acids 1-24



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## FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT  
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
 GTCCGCCTGGAGGTCACCGAEGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCGGG  
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA  
 CGGGCCCCCTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGCTGGAGGTCGCCGACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC  
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCAG  
 ACCCCACACTGGCGCGCGGCCACAACGTCAATGTCATCGTCCCCGAGAGCCGAGCCCAC  
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC  
 TGTCTCCTGGCCGCCCGCAGGCGCCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA  
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT  
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT  
 GCAAA**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCT  
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC  
 AAAATCCCACTGATGCCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCCTG  
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAACTGGGGTCAGCCTCA  
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA  
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT  
 CCTCCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
 CTTTGGGGCACCTGGGGCTGCACCCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT  
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA  
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT  
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTTAAAAAAA  
 AAAAA



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## FIGURE 47

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCGAC**ATG**GCCGTTGTCTCAGAGGACGACTTT  
CAGCACAGTTCAAACCTCCACCTACGGAACCAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT  
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT  
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA  
GGACCCTGAGGGCTCAGACATCCTGAACCTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
TGCCCTCCATGCTGTGCCTGGTGGCCAACCTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC  
CGTGCTCCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACCTGGTGAA  
GGTGGACACTTCCTCCTGGACCCGTGGTTTTTTTTGCGGTCACCATTTGTCTGCATGGTGATCC  
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTCTATG  
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCCTGACGG  
CCACCATCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
AGGTACTACATGAGGCCTGTTCTTGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA  
GGACTCCCTCAGTGCCCCCTTCGGTGGCCTCCAGATTGATTCCACACACCCCCCTCTCC  
GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCACC  
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACCTTGTGACCTAT  
GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGG  
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACCTACCAGCCCCGCGT  
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG  
GGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG  
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG  
CTCAGCCTGCTCTACCCCTCCTGGTGCACCTCATC**TAGA**AGGGAGGACACAAGGACATTGGTG  
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC  
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA  
GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAACAGAACACT  
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA  
ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCCGCCCTAGAGTTATTACA  
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCT  
GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA  
AGTCCCCTGGCATGGTCAGTCCTCAGGCCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
GCGGGTGAACAACTGCCCACTAACCAGACTGGAAAACCCAGAAAGATGGGCCTTCCATGAAT  
GCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC  
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
GTATTCAAAAA

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## **FIGURE 48**

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYIIFFSLGI  
GSLLPWNFFITAKEYWFMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY  
LLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF  
CVTYVFFITS LIYPAVCTNIESLNKGSGLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL  
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

### **Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
305-330, 448-472



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## **FIGURE 50**

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSSEDGFFYLSFAEALR  
AHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL  
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG  
HSNTDRPSRMIFYPPPREGALLLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

## FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT  
GGAGCGCTCTGAAGCCACCCTGTCTCTGGAGGAACCACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA  
 GAACTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCCCT  
 GCTGCTGTTTACAAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCCACTTCCGACCCCGGCGTTGATCTGCAT  
 CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGCTTACCTCTTCTTGACCTGAA  
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTCCAGAAGAACAATGACCTAACAAAGTTGCTG  
 CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG  
 ATATAGAAAACCAAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTC  
 CTGTCTCTTGCAATAAAGTTATAAATCATCACCAGACCAGTTTGTCTGGCATCTTTGCTCAGAATAGGCCAGAGTG  
 GATCATCTCCGAATTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC  
 CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT  
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA  
 GCAAAGAGGGGAGAAGAGTGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCA  
 AAAACCTGTGCCTCCTAGCCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG  
 AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCC  
 CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA  
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
 CACATTGTTTTCCCGCGGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCTT  
 GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
 TTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTGTCAGTGGAGC  
 TGCCCCCATGTCCACTTCAGTCATGACATCTTCCGGGCAGCAATGGGATGTCAGGTGTATGAAGCTTATGGTCA  
 AACAGAATGCACAGGTGGCTGTACATTTACATTAACCTGAGTACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
 CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG  
 GCTTCACACAGGAGACATTGGTTCGCTGGCTCCCGAATGGAACCTCTGAAGATCATCGACCGTAAAAAGAACATTTT  
 CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAGTGTTACA  
 AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCCCTGACACAGATGTACTTCCCTC  
 ATTTGACGCCAAGCTTGGGGTGAAGGGCTCCTTTAGGAACTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT  
 AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAACTTTTTGAACAGGTCAAAGCCATTTTTCTTCATCC  
 AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT  
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCCACTG  
 TGCATGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTTGCCTTTCCCTCCTATTTTTTTTTTAACC  
 TGTTAAACTCTAAAGCCATAGCTTTTTGTTTTATATTGAGACATATAATGTGTAACTTAGTTCCCAAATAAATCA  
 ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA  
 GATCCCAGTTTATGTTCTGTGTCTTCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT  
 CAAAGGGACCCTCTGTGCCTTCTTCTTTGTTTTGTGATAAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA  
 TCTTCTACTGTTCAAATAAGAGATTTTTAAATTCTGAAAACTGCTTACAATTTCATGTTTTCTAGCCACTCCAC  
 AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT  
 CTGCGTAAATTAAATTGTGTACTGAAGGGAAAAGTTTGATCATACCAAAACATTTCTTAACTCTCTAGTTAGATA  
 TCTGACTTGGGAGTATTAAAAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA  
 CAGTAGGAACCTGGGGAGTAAATCTGTTCCCTACAGTTTGTCTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA  
 GGTGGGCCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAAAACCTCCTGAACCTGGGAACAAAGATCT  
 ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTTCTGTGAAGGAACCAACTGATCTCCCCACCCTTGGATT  
 AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAATAAAC  
 TATTACAGATAAAAAA

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## **FIGURE 52**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFKLLFTKMLFIFN  
 FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNQSVGIEGGARKGVVSQKNNDLTS  
 CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS  
 PDQFVGIFAQNRPEWIISELACYTYSMAVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL  
 VLIGNVEKGFPTPSLKVIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED  
 LSVICFTSGTTGDPKGAMITHQNIVSNAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQ  
 AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAPVRLNRIYDKVQNEAKTPLKKFLLKLA  
 VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVY  
 EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK  
 GYLKDPEKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNI FKLAQGEYIAPEKIENIYNR  
 SQPVLQIFVHGESLRSSLVGVVVPDTPVLPFAAKLGVKGSFEELCQNQVVREAILEDLQKI  
 GKESGLKTFEQVKAIFLHPEPFSEIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

**Important features:**

**Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622



**FIGURE 53**

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## FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVIVNIKLILDTR  
 RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA  
 REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK  
 DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDVPVLLKTDVPLSS  
 AEEAECHWADTELNRRRRRFC SKVEGYG SVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN  
 RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEYEEPMDVVALFGLRGIQHTPISIKNARVSQHY  
 KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA  
 EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMMRMPEQRRGRECIIPDVS  
 RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVD SLKKEAYEVEVHRL LSEAEVLDHS  
 KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDL DVRGNHRGLWRLFRKKNH  
 FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

### Important features of the protein:

#### Transmembrane domain:

amino acids 38-55

#### Homologous region to Mouse GNT1

amino acids 229-660

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**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACAC  
 CTGTTTAAAGAACCTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA  
 AAGGAGGGCAGAAATGGGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA  
 CGTGGCCGGAATCATTCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGAATGTTTGG  
 GTGCTGGCCTTCTCTGTGGAACCTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTATGAA  
 GATATTCTTGAGGGAAAACACCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAAAGCAGC  
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCTATATTGGTG  
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT  
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAAATCACCACCACGCTGGGTCTGGTTGTCCA  
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG  
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT  
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT  
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG  
 CCATGCTTTTCTCTGCGGGACATTTCTTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGCGGA  
 ATAGGGCACAGCCACAAGCCGATGCCACGGGAGGGAGGCCCTCAGCCGCCTGGAAGTGGCAGCCCT  
 GGTTCTGGGTTGCCTCATCCCTCTCATCTGTCTAGTAGGACACCAGCATTAAATGTTCAAGGTCCAGC  
 CTTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTTCCTCAGTC  
 TCTTGTCTCACCTTGCATCTCTACATGTATTCCTAGAGTCCAGAGGGGAGGTGAGGTTAAAACCTG  
 AGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTGTGT  
 TATCTTTTAAAGGCCCTTGACATTTTGCGTTTTAATATTTCTCTTAACCCTATTCTCAGGGAAGATG  
 GAATTTAGTTTTAAGGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAAATACAGT  
 GTTCTGTAATTAAGCTATGTCTCTTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT  
 AACATGGTTCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA  
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC  
 AAGACACATTGAAAGCTCTCTTATACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT  
 TAAACAGCTCCTTTGGCACGTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG  
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCCTTGTCAGTTCTCCTTTGCAGAAT  
 ACCTGTCTCCACATTCTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCTTCAAGAA  
 CAGTCAGATCACAAAGTGCTTTTGGAATTAAGGGATATTAAATTTTAAGTGATTTTGGATGGTTAT  
 TGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAAATGTATGGTTGTCCTTTTTTTTTGTTTTT  
 TTTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTGAGCTTT  
 GGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTTGCCTA  
 TTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGTCTTTTCTTTGCTTTTCTTCTAACTTT  
 TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAATT  
 CTTATCAGGACAACCACCTTCTCGAACTGTAATAATGAAGATAATAATATCTTTATTCTTTATCCCCTT  
 CAAAGAAATTACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAATACCACCTCCTCATGTGTAA  
 ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATA  
 ATTTTTTTTTTTCATATTTGCCAAAATTTTGTAAACCCTGTCTTGTCAAATAAGTGATAATATTGTAT  
 TATTAATTTATTTTTACTTTCTATACCATTTCAAACACATTACACTAAGGGGGAACCAAGACTAGTT  
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTA AAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATG  
 ATTTATTTCCCTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTTGTGAGCCCTCTGCT  
 GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCATACA  
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT  
 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACCTATATGGTTGCCTAGATTCTCTCTGGA  
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAAA

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## **FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ  
IGNSHVHSTDDPEAARSSNSKITTTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHELLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

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## FIGURE 57

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC  
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG  
GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC  
ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGACCTCCAGACACGGAT  
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGA  
AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAA  
TAACATCACCACAGGTGAGAGGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA  
GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG  
AGGAAGTTCTCCTACGACCTGAGCCAGTGATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
TGAGGAGCGAATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAA  
GTCCCAGACACCAGCCCCCAGTTCCGAAGTGGTTTTTGGATTCAAAGAGACAAGTTGAGAAAG  
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
CCAGGCCGGGAGCAGGTGGTGGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
AGAAGTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA  
TGGAGGGCCCTGAGCGAGACCAGCTTGTTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG  
TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG  
AATCATACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA  
TAAAATGTTTCATGAGGGACTGAATACTGAAAATGTGAAATGTACTAAATAAAATGTACATCTGA

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## **FIGURE 58**

MMGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNDQRQQQLQALSEPQPRLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR  
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

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**FIGURE 59**

GGATGCAGAAAGCCTCAGTGTTGCTCTTCCTGGCCTGGGTCTGCTTCCTCTTCTACGCTGGCATTGCCCTCTTCA  
 CCAGTGGCTTCCTGCTCACCCTTTGGAGCTACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC  
 TGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGGGGTTGTGTTGGTGCTGA  
 TAGATGCTCTGCGATTGACTTCGCCCAGCCCCAGCATTACACGTGCCTAGAGAGCCTCCTGTCTCCCTACCCT  
 TCCTGGGCAAACCTAAGCTCCTTGACAGAGGATCCTGGAGATTACAGCCCCACCATGCCCGGCTCTACCGATCTCAGG  
 TTGACCCTCCTACCACCACCATGCAGCGCCTCAAGGCCCTCACCCTGGCTCACTGCCTACCTTTATTGATGCTG  
 GTAGTAACCTTCGCCAGCCACGCCATAGTGGAAGACAATCTCATTAAAGCAGCTCACCAGTGCAGGAAGCGTGTAG  
 TCTTCATGGGAGATGATACCTGGAAAAGACCTTTTCCCTGGTGCTTTCTCCAAAGCTTTCTTCTTCCCATCCTTCA  
 ATGTGAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCCACCATGGACAGTGGTGAATGGG  
 ACGTGCTGATTGCTCACTTCCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCTGAAATGGCCA  
 AGAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG  
 CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTAGCTGCTCTCTTTC  
 TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCCACCAGAGGAGCCAGAGGTGATTCTCCTCAAGTTAGCCTTGTG  
 CCACGCTGGCCCTGCTGCTGGGCCTGCCATCCCATTTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG  
 GGGGTGAGGACTCCAGCCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT  
 CCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT  
 TCTCCAAGGCCTCTGCTGACTACCACTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA  
 TTGCTGAGCTGCAGCAGTTCCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC  
 GCATGGCGGGGGTACTGCTCTCTGGCTGCTTCCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC  
 CAGGCTTTCCATTCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGGGGCCATAGCGTATGCTGGAC  
 TCCTGGGAACCTATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCTCCCTT  
 TTCTGTGGAAGCCTGGGCTGGCTGGGGGTCCAAGAGGGCCCCCTGGCAACCCTGTTTCCCATCCCTGGGCCCCGTCC  
 TGTTACTCCTGCTGTTTTGCTTGGCTGTGTTCTTCTCTGATAGTTTTGTTGTAGCTGAGGCCAGGGCCACCCCT  
 TCCTTTTGGGCTCATTCTCCTGCTCCTGGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC  
 TCACAATGCCCCGCTTGGCACTTCAGCCACAACAACCCCCACGGCACAATGGTGCATATGCCCTGAGGCTTG  
 GAATTGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGCCACT  
 CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTTCGAGCCAAGAATTTATGGTATGGAGCTTGTGTGG  
 CGGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCCGCTATGGTAATCTCAAGAGCCCCGAGCCAC  
 CCATGCTCTTTGTGCGCTGGGGACTGCCCTAATGGCATTTGGGTACTGCTGCCTACTGGGCATTGGCGTCGGGGG  
 CAGATGAGGCTCCCCCGCTCTCCGGTCTCTGGGCTCCATGGTGTGCTGCCTCGGGCTGTAGCAGGGC  
 TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGCTGGTGAAGGCTGGGGCAGGCGCTCCAA  
 GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAAA  
 TCTACCGACACATGCAGGAGGAGTTCCGGGGCCGTTAGAGAGGACCAATCTCAGGGTCCCCGACTGTGGCTG  
 CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTACAGCCCTCACCCCTGTTGGCCTTCCCCTTCTGCTGT  
 TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCAGAGCTTCCTTCTCCTACATCTGCTTGCTG  
 CTGGGATACCCGTCACCACCCCTGGTCTTTTACTGTGCCATGGCAGGCACTCTCGGCTTGGGCCCTCATGGCCA  
 CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTCCAGCCATCCATTTGGCATGCAGCCTTCGTGGGATTCC  
 CAGAGGTCATGGCTCCTGTACTTGGCTGCCTGCTTTGCTAGTGGGAGCCAACACCTTTGCCTCCCACCTCCTCT  
 TTGCAGTAGGTTGCCACTGCTCCTGCTGCTGCTGCTTCTGCTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC  
 CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG  
 ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCTCAAGTACCTCTTTATCCTTGGTATTTCAGATTC  
 TGGCCTGTGCCTTGGCAGCCTCCATCCTTCGCAGGCATCTCATGGTCTGGAAAGTGTTTGGCCCTAAGTTTCATAT  
 TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGTGAGAGTGGATGGTG  
 CTGTGAGCTCCTGGTTTCCAGCAGCTATTTCTGGCCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT  
 ACAGAGAGTGCTGGAGAACAGTGATAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC  
 TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTAGGACCACAGTGGAGTA  
 TGATCCCTAATCCTGATTTGGATGCATCTGAGGGACAAGGGGGCGGTCTCCGAAGTGAATAAAATAGGCCGG  
 GCGTGGTGACTTGCACCTATAATCCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA  
 AGACCAGCCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAAAGTGAATAAAATGATAATAT

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## **FIGURE 60**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPPGPGSLPWGSQGKPGACW  
 MASRFSRVVLVLIDALRFDFAPQHQSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ  
 VDPPTTTMQRLKALTTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF  
 PGAFSKAFFFPFSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHHPHPEM  
 AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAALFLYSPTAVFPST  
 PPEEPEVIPQVSLVPTLALLLGLPIPFNGIGEVMAELEFSGGEDSQPHSSALAQASALHLNAQ  
 QVSRFLHTYSAATQDLQAKELHQQLNLFASKASADYQWLLQSPKGAEATLPTVIAELQQFLRG  
 ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGFPPFCPLLLTPVAWGLVGAIA  
 YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFIPIPGPVLLLLLLFRLA  
 VFFSDSFVVAEARATPFLLGSFILLVVLVQLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY  
 ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA  
 AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAAYWALASGADEAPRRLRVLVSGASMVLV  
 RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE  
 EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL  
 LLHLLAAGIPVTTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAFVGFPEGHGS  
 CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLCESQGLRKRQQPPGNEADARVRPEEEEEEP  
 LMEMRLRDAPQHFYAALLQLGLKYLFI LGIQILACALAASILRRHLMVWKVFAPKFIFEAVG  
 FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Transmembrane domains:**

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
 1016-1034, 1052-1070

#### **Leucine zipper pattern.**

amino acids 843-864

#### **N-glycosylation sites.**

amino acids 37-40, 268-271



# FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT  
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**  
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT  
 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA  
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
 ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG  
 CCCATATCTATTACCGTGTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAA  
 GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACCTTTATCACCCCTCAATATCTCGGATGAT  
 TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA  
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
 GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT  
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAAACAGTCATTGAATATGA  
 ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG  
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCG  
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA  
 CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC  
 AAACCTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTTCAGAGGGCTGCGAG  
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT  
 TATATGTGCAGATGGAAAAC**TGA**TGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAAC  
 AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGT  
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG  
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT  
 TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTTCAGG  
 TGGGTGT

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## FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ  
 QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ  
 CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYIGNEFD  
 KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH  
 LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEYDVRTTDICAGPEEQELSL  
 QEEVSTQGTLLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD  
 PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW  
 GLYVQMEN

### Important features:

#### Signal peptide:

amino acids 1-28

#### Transmembrane domain:

amino acids 140-163

#### N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

# **FIGURE 63**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT  
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCCAGATCATCGGGGGCCACGAGG  
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCCAACATCACTGCGGA  
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT  
CCGCACTGGCCTGGTGGTGTGCTGGGCGCCACGTCCTGAGTACTGCGGAGCCCACCCAGCAGG  
TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC  
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT  
TCGTGTCTGACTTTGAGGAGCTGCCGCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC  
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG  
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGA  
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCCGAC  
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC  
CCAGCCCCGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT  
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG  
AAGCCTGATGTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA  
AAGGGCAGAAGCAAACCCAGTAAATGTAACTGACAAAAAAAAAAAAAAAAAAAAAGAAA

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## **FIGURE 64**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF  
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDIC  
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD  
VCNSSWKGHLTLTMLCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY  
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

**Signal peptide:**

amino acids 1-30

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## FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  
CGCCTGTCCCCGGCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG  
CAGGCGCCGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAGGCCACC  
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT  
GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
CGGCAGCAAAGGACATCCGCGGGGAGACCCCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT  
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT  
TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC  
AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG  
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT  
GCCAGAGCAAGCTCGCCATCGTCCTCTTCACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT  
GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
CATCCATGGCTCCACCTTCTCCAGCACCACACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA  
GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAACTGGCGGATGTT  
TCCGGAAAGTACTTCGATGGACTCAAACAGAAAGCCCCCGGCCCGAGGCTGAGGATGAGGA  
GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA  
GGGAGCAGCCCCCTCCCCAGAT**TAA**CCCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG  
ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCACTACCTGAGCCGGGAGACCCAG  
GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC  
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG  
AGGGGCCATCTGATGCTTCCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
TGTGCACTTGCAGGCCACGTCAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC  
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG  
CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG  
GGTGTCTTGTGAGGGCTTCCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTATCCC  
GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACAGCTGCTGCTACAGGACCTGGGA  
TTGCCTGGGACTCCCACCTTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC  
TTGCTCATTT

amino acids 1-17

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## FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTTGGGGCGCGGCTGGCGGGCGCTGCTGGCGGTGCTG  
GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGGCGCTGAC  
CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGTCAT  
GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCAAACGCCTGCA  
GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT  
TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTCTTTTCTCTCA  
CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC  
ATTCCATGGCTGGAGGAGGCTGTGAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA  
GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA  
ATGTTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG  
ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC  
TGAGGCTGTATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
TATGTCAGACCCTGGGTTCACAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCCTAT  
GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCATCCACCTGGA  
GCCCTACATTGCTCTCTACCATGACTTCGTGAGTCACTGAGAGGCTCAGAAAATTAGAGAAC  
TTGAGAACCATGGCTACAGAGGTGAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCTCAA  
CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG  
TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTACCAAGC  
AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
GGTGGAAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA  
ATGCAGCACTGTTTTGGTGGAAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
GCTGGCTGTCCTGTCTGGTGGGAGATAAGTGGTGGCCAACAAGTGGATAACATGAGTATGG  
ACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAGACT**TGA**ACTGTTGGCAGAGAGAAGC  
TGGTGGAGTCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA  
AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCCTCGCAAATCAGAGGC  
AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA  
GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGGAAGTTTCTGG  
AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTC  
TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG  
GGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG  
CAGGGAGTGTCCCCCTCCCAGAAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTT  
TTTAAGTTGAAAACAACTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAA  
ATGTTTATAAATCAAAA

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## **FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEARL  
 RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
 QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVTGSAITDLYSPKRLFSLTGDDCFQ  
 VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS  
 LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRDTYEGLCQTLGS  
 QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
 RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
 GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW  
 NLHRSGEGSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19



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## FIGURE 69

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG  
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG  
CGCCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
TGGCTCAAGTTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT  
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC  
TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT  
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTCATGTACATCCTTGGGAT  
CTGCCTCATCATGGAGCTCATTTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG  
ACTTCCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
AACATCATGGACTTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
GAGCAAGAATCAGTACCACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA  
CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATATCGAC  
AAGGAGCGTTTCAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT  
CTGGTTTCATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT  
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC  
TCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG  
ATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACACA  
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC  
CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT  
GCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
GAGCCTGAGGCTCTGCTCAGGGCCCATTTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA  
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTCGCCCTCGGGGCAGGAGGGAAGG  
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTGGC  
CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA  
GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC  
TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTTAA  
TCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAAAA

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## **FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP  
 AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL  
 NDNIRRGIE NYDDLD FKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGV PYTCC  
 IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVI IW FMDNYTIMACILLGILLPQFLG  
 VLLTLLYITRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN

### **Signal peptide:**

amino acids 1-44

### **Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

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## FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA  
CACCTGGGAAGATGGCCGGCCCGTGGACCTTCACCTTCTCTGTGGTTTGCTGGCAGCCACC  
TTGATCCAAGCCACCCTCAGTCCCAGTGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGA  
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC  
GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
ACACGCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC  
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCA  
TGGGAGCCTGCGCATCCAACTGCTGTATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGC  
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG  
ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT  
CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT  
AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC  
TCTGCAGCTTCCCTGACAATGCCACCCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA  
GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCTGTTGG  
ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT  
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTCCTCCA  
GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC  
ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
GAACTCTGGGATTTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG  
AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC  
AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCCAGTGAAGACTTGGATGGCAGCCATCAG  
GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
CAATAAACACTTGCCTGTGAAAAA



## FIGURE 73

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTATCTGA  
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
 CTCCAACCTGCATAGACAGTGTGTGCTTTGCAAGCAAGCTGATGAAGAATTCAGATCCTGGC  
 AAACCTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGGCCATGGTGGATTTTG  
 ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTCAGCTCCAACTTTCATCAACTTT  
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC  
 TGAGCAGATTGCCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT  
 CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAAACTGGATGGGCTTTTGCAGCTTTGTG  
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA  
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCTTTTATG  
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTTCTGATGAGTTAAAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAAATCGTGTGTGTTTGAAAAGAAGAATGCAACTTGTATATTTTGTATTAC  
 CTCTTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAGAAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT  
 CCCAGTGAACCTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTAAAA  
 CTACTACTTTGTTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT  
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC  
 TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
 ACTTTACGCATCTTTCTTTTGGAGTAGAGAAATTATGTGTGTCATGTGGTCTTCTGAAAATG  
 GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA  
 GATTTTCAGATTCATTCCATCTCCTTAGTTTTCTTTTAAAGGTGACCCATCTGTGATAAAAATA  
 TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT  
 TTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC  
 GAGGTCAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT  
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

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## **FIGURE 74**

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRPFVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG  
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPSFLMS

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

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## **FIGURE 76**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFDGRLTFHPGSQVVKLPFINF  
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ  
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW  
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVS HDAIKIPKWSPLS  
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY  
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL  
PQNLSGYSL LPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS  
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG  
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501

#### **Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97



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## **FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATC**  
 GCCTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
 GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG  
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCCAGGCCATGAT  
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
 CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC  
 ATCCTTGGAGGCCTCCTGGGATTCATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA  
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCC  
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC  
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT  
 ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTCAGAAGGTGCTGCTGAGG  
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG  
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC  
 CCCTGCCCTAAGTCCCCAACCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG  
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTG  
 ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
 TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC  
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

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## **FIGURE 78**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886

><subunit 1 of 1, 230 aa, 1 stop

><MW: 24549, pI: 8.56, NX(S/T): 1

MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT  
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF  
FILGGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS  
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

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## **FIGURE 79**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATGG**TGCCCAGAATCTTCGCTCCTGC  
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG  
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG  
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC  
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTG  
TGAAGCTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTTCC**CGA**GAAGACATAGAAAGAAAATCAACTTTCTACTAAGGCATC  
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG  
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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## **FIGURE 80**

MVPRI FAPAYVSVCLLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE  
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25

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## **FIGURE 81**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA  
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGCAGTGTCAGCTTAATGGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACCTTCATT  
CTGTGACCTGTCTGAGGCCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCTTCACCCT  
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

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## **FIGURE 82**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Signal peptide:**

amino acids 1-24

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## FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG  
TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCGGCACCAGAAGTTCCTCT  
GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTGCG  
CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTACCCTCACCTGCAGGCTCT  
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
GGCGAGGTGCAGACCTGCTCAGAGCGCCGGGCCATCCGCAACCTCACGTTCCAGGACCTTCA  
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG  
GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT  
CCATGGTGGCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT  
ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
CTCCAACCGCCGTGCCCAGGAGCTGGTGCGGATGGACAGCAACATTCAAGGGATTGAAAACC  
CCGGCTTTGAAGCCTCACCACTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCCTG  
TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC  
CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT  
CTCCAAACTTTGAGGTCATCTAGCCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC  
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCCTCAACCCCTC  
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGCTGAG  
ATTCTCCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG  
GAGAGACTTCTCCCCCGTGGCCGCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC  
AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC  
ACCTTCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
ATGTTGCCCCACCACTGGAGATGGTGTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA  
GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCCTGCTCAGCGCGGGCC  
ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT  
GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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## **FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFQVATPYSLYVCPEGQNVTLTCRLLGPVVK  
GHDVTFYKTYWRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD  
HHGNFSITMRNLTLTLDGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ  
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

### **Signal peptide:**

amino acids 1-28

### **Transmembrane domain:**

amino acids 190-216



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## FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT  
 TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCC  
 TTTCTGCCCCACGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG  
 GGTCTGTGGGTTGATCTGTGGCCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGA  
 CTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGG**ATG**GTTCCTGAGGTGAGGGTCCTC  
 TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC  
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT  
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT  
 TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG  
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGGCCCCACCAAAGTCCTGCC  
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC  
 CGCCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC  
 AACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCCTGCCAGACTCCTGCTGCCAAGCCT  
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG  
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGGCCGGGCACCCACAGC  
 CCCCCTGGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG  
 GCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG  
 AAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG  
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT  
 ACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAA  
 GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCTT  
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG  
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG  
 AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA  
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC  
 GAAGGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGA  
 CAAAGTGACCAAGACATAACAAAGACC**TAA**CAGTTGCAGATATGAGCTGTATAATTGTTGTT  
 ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 86**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPFDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT  
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDPCSSDAGRKRGPPTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKVGAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLLWKL  
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPARRSLERLPSDPDG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

[illegible]

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## **FIGURE 88**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGGEGGASGRSP

**Signal peptide:**

amino acids 1-18

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## FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAAGCTAACCCCTCGGGCTTGAGGGGAAGA  
GGCTGACTGTACGTTTCCTTCTACTCTGGCACCCTCTCCAGGCTGCC**ATG**GGGGCCAGCACC  
CCTCTCCTCATCTTGTTTCCTTTTGTTCATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCT  
TGTGGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCAGTGCCAGGACC  
AGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAG  
GTGGCAGAGAAGGAGCGGGAGGCACTCAGAAGTGAAGCCGACACCATCTCCGGGAGAGTGGA  
TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTGTAGAGT  
TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAGAAGGAATGAGAAGTAC  
GATATGGTGACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG  
ATTTGGTGGCCAGCTGGTCTATGGACCAAAGGATCCACTGGGGCAAACAGAGAAGATCTACG  
TGTTAGATGGGACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCTT  
GCCATGGCTGCCCCGAAAGCTTCCCGAGTCCGGGTGCCCTTCCCCTGGGTAGGCACAGGGCA  
GCTGGTATATGGTGGCTTTCTTTATTTTGTCTCGGAGGCCTCCTGGAAGACCTGGTGGAGGTG  
GTGAGATGGAGAACAACCTTTGCAGCTAATCAAATTCACCTGGCAAACCGAACAGTGGTGGAC  
AGCTCAGTATTCCCAGCAGAGGGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACAT  
CGACCTGGTAGCTGATGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGC  
ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACCA  
TGTCACAGAGAGAATGCTGAGGCTGCCTTTGTTCATCTGTGGGACCCCTCTATGTCTCTATAA  
CACCCGTCTGCCAGTCGGGCCCGCATCCAGTGCTCCTTTGATGCCAGCGGCACCCTGACCC  
CTGAACGGGCAGCACTCCCTTATTTTCCCCGCAGATATGGTGCCCATGCCAGCCTCCGCTAT  
AACCCCCGAGAACGCCAGCTCTATGCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGA  
GATGAGGAAGAAAGAGGAGGAGGTT**TGA**GGAGCTAGCCTTGTTTTTTGCATCTTTCTCACTC  
CCATACATTTATATTATATCCCCACTAAATTTCTTGTTCCCTCATTCCTCAAATGTGGGCCAG  
TTGTGGCTCAAATCCTCTATATTTTGTAGCCAATGGCAATCAAATTCCTTCAGCTCCTTTGTT  
TCATACGGAACCTCCAGATCCTGAGTAATCCTTTTAGAGCCCGAAGAGTCAAACCCCTCAATG  
TTCCCTCCTGCTCTCCTGCCCCATGTCAACAAATTTAGAGGCTAAGGATGCCCCAGACCCAGG  
GCTCTAACCTTGATGCGGGCAGGCCAGGGAGCAGGCAGCAGTGTCTTCCCCTCAGAGTG  
ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCTCTGTCCTCTCTCCTCACTCCTCCCT  
TCAGTGTCTGAGGAACAGGACTTTCTCCACATTGTTTTGTATTGCAACATTTTGCATTAAA  
AGGAAAATCCACAAAAA  
AAAAA

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## **FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM  
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVRVFPFWVGTGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN  
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTAQ  
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 177-180, 248-251

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## FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG  
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT  
CCGTACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTC  
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG  
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
ACAAAAGTGGTGAAGGATTCTATTGCGGAGGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC  
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA  
TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCCTCTCATTTCCATCACGGGATATGTT  
GATAGAGACATCCAGCTACTCTGTGAGTCCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG  
GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG  
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA  
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAAGTGGAC  
TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC  
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAAGTGTAAACCCATA  
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG  
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGGTCTTCCTGGACTATGAGTG  
TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT  
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAAGTCCC  
ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC  
AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGGG  
GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA  
GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC  
ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT  
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG  
TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA  
AAAAAA

**Signal peptide:**

**Transmembrane domain:**

amino acids 239-255



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## FIGURE 93

GCGATGGTGC GCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCA  
ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC  
**CATG**AGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG  
CCGTGCGCTCAGCCGCCCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCAGGTG  
GACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCCCAGCCACCCCTTCCCTAGGGCGACGGC  
TCCCACGGCCCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG  
CGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC  
ACCACCTTTTCAGGCGCCGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTC  
GACCACCTCTCAGGCGCCGACGACCCGCGCCGACCAACCCCTTTCGACGACCACTGGCCCCG  
CGCCGACCAECCCTGTAGCACCACCGTACCGGCGCCACGACTCCCCGACCCCGACCCCC  
GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCTCTC  
TTCGCTCCTCCAGAGTATGTATGTAAGTGTCTGTGGTTGGAAGCCTGAATGTGAATCGCT  
GCAACCAGACCACAGGGCAGTGTGAGTGTGCGGCCAGGTTATCAGGGGCTTCACTGTGAAACC  
TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCC  
ACATGGAGCTCTCAGCATAACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAAGTGAAGTTTATT  
TTATTTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTCTTACTTTATATGT  
TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAAGCACTAG  
AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGAAT  
AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT  
ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTCTCTCTA  
ATCAAAATTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA  
TTTAACTAGTGGAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTTGAGACCAAAAG  
TAGATTAAGCAGGAATTATCTTTAAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA  
ATAATGTACTGTTATCTAAGCATTGCGCTTGACTGCACTGAAAGTAATTATCTTTGACCT  
TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAAT  
AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC  
CACTTACGAGCTGTGTTCTTTGGGCAAGTAATTTCTTTCACTGAGCTTGTCTTCTCAAG  
GTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA  
TTCTGGTTTGTTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA  
ACTTTTAGCTCCTTGACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTA  
TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAAAAATGTAGAAG  
AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT  
CACTTGAGGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA  
AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT  
GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT  
GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 94**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

MRSLSLGGGLALLCCAAAAAVASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATA  
PTAQAPRTGPPRATVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSPTTPPAAERTS  
TTSQAPTRPAPTTLSTTTGAPPTPVATTVPAPTTPRTPTPDL PSSSNSSVLPTPPATEAPS  
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLN YTSGLCQPCDCSP  
HGALSIPCNR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

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## **FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC  
CTGGGCTTCTGTGTCACAG**TAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT  
CACAGCA

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## **FIGURE 96**

MGGLLLAAFLALVSVPRQA VVLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20

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## FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCTGCC  
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
 CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
 GGCTGGATTTACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA  
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA  
 AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG  
 GCACCCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG  
 GGGACACCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
 CCGTCTCTCGGTGCTCACCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC  
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG  
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC  
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
 ATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
 AGAGCAAAGCCACATCAGGAGTGAATCAGGGGGTGGTCCGGGGGAGCTGGAGCCACAGCCCTG  
 GTCTTCCTGTCCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGTCAGGAAGAAATCGGCAAG  
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTTCAGCCT  
 CTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAAGACAGTCCCCCAGACCAGCCTCCCCAGCT  
 TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
 ACAGATGAAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGA  
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
 CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

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## **FIGURE 98**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF  
 REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
 SIKWNYKHHRLSVNVLTALTHRPNILIPGTLESGCPQNLTCVSPWACEQGTPPMISWIGTSVS  
 PLDPSTTRSSVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLMTVFQGDG  
 TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
 HLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
 CRKKSARPAAGVGDTGIEDANAVRGSASQGPLEPWAEDSPDQPPPASARSSVGEDELQYA  
 SLSFQMVKPWDSTRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

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## **FIGURE 99**

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATGA**AAGACCCTGTTTCCTG  
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCAGGA  
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTCACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC**TAGG**  
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT  
TTTCCCCCAA

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## **FIGURE 100**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVVDKDFPEDRRPRKVSPVKVTALGGGKL  
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH  
MGKLVGRNSDTNREAL EEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

**Important features:**

**Signal peptide:**

amino acids 1-17



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## FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA  
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTCGAG  
 TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGC<sup>1</sup>ACTCTGTGG  
 GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA  
 TAGTTCACCTGGGGCAGCACAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA  
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC  
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC  
 AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTTGAGCACCA  
 GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTT  
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATACCCGAAAGCCTGGTGTCTACAC  
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA  
 CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACCTCTGTTAAT  
 AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG  
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT  
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA  
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 102**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH  
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV SITW  
AVRPLTLSSRCV TAGT SCLISGWGSTSSPQLRLPHTLR CANIT IIEHQKCENAYPGNITDTM  
VCASVQEGGKDSCQGD SGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

### **Important features:**

#### **Signal peptide:**

amino acids 1-18

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

#### **N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

#### **Glycosaminoglycan attachment site.**

amino acids 145-148

#### **Kringle domain proteins.**

amino acids 197-209, 47-64

#### **Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

#### **Apple domain proteins**

amino acids 222-249, 189-222

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## **FIGURE 103**

GAGCAGTGTTCTGCTGGAGCCG**ATG**CCAAAACCATGCATTTCTTATTCAGATTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA  
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCCTTCATT  
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG  
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAAGATATTTTGA  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT  
GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTCCCCTATGAGAAGATATTTTGA  
TCTCCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 104**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG  
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY  
AEGKIIPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD  
KSYQDAVLEDIFKKNDHDGDFISPKEYNVYQHDEL

### **Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214

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## **FIGURE 105**

CAGAA**ATG**CAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT  
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCCAGTTCTTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC  
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTTCTTGTTTCATTTGCGGACTGCCCTCTCAGTGTTTCCTGGGATCCCCTCCCAAATAA  
AGTACTTATATTCTC

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## **FIGURE 106**

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL  
ETCNARHGG SRL

**Signal peptide:**

amino acids 1-18

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## **FIGURE 107**

CAAGCAGGTCATCCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC  
AGGGAAAGGGTGACCTCTGAGATTCCCCCTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**  
GGCTCAGCATCTTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC  
CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTTCACAGCGGCTCACTGCA  
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA  
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC  
CCCTGCCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC  
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT  
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG  
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA  
GTCCTTCAAGGTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**  
CTGTTTCCTCCACCTCCACCCCCACCCCTTAACCTGGGTACCCCTCTGGCCCTCAGAGCACC  
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACCTT  
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA  
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

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## **FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGVPCGQDGI PGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17



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## FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA  
ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC  
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC  
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
AAGATGATCTCAGAGGTGACAGGAGGGGTCACTGACACTATATCCTACCGAGACTTTGTGAA  
CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCC**TGA**  
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT  
CTTGACACACTGTGATCTCTCTCTCTCATTGTGTTGGTCATTGAGGGTTTGTGTTGTGTTT  
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTTCGGGGAATCC  
TGAGCCTTGGGTCCCTCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG  
ATATCAAACCAAAAAGTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
CTCACTTGAGGAACCAAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC  
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
TACCAGAAGGAACCCTCCAGTCCTGCTCTTGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAAGTGAGGCCTG  
GGGTTTGGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
CTGAGAAATACAAGGTTGCTTGCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

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**FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEinREFLCDQKYSDEENLPEKLTAfKEKYMEFDLN  
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVM  
MFEGKANESSPKPVGPPPERDIASLP

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## FIGURE 11A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCAGAGGCAGCCTCCTCCA  
GGAGCGGGGCCCTGCACACC**ATG**CCCCCGGGTGGGCAGGGGTGGCGCCGCCGTGCGCGCC  
CGCCTGGCGCTGGCCTTGCGCTGGCGAGCGTCCTGAGTGGGCCTCCAGCCGTGCGCTGCCC  
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTT  
CTCGGGGCATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC  
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGTCATCTGGAAGACAACCAGGT  
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA  
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA  
GATTTGAGTGAAAACCAGATCCAGGGGATCCCCGAGGAAGGCGTTCCGCGGCATCACCAGATGT  
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCTTGGTCACCGC  
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG  
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT  
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG  
TGCCCAGCCCCCACTCGGAGCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCC  
CTGCACGTGCAGCAATAACATCGTGGACTGTCGAGGAAAGGGCTTGATGGAGATTCTTGCCA  
ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA  
GGAGCCTTCACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA  
TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA  
AGATCACCAGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC  
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT  
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGT  
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG  
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCGCGCTGCAGCAGCCCGCGCCG  
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCGCTGCTCAGGCTCCGAGG  
ATTACCGCAGCAGGTTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG  
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC  
TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
CGAGAGGGAGCTTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT  
GGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA  
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGTGAGACTGCTG  
TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCACCACGCTTGTCTCCCT  
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA  
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTTCTC  
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
TAGCTGCCAGCTGAGCCCGCGCTGCCCCGAGCAGTGCACCTGTATGGAGACAGTGGTGCAT  
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC  
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT  
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC  
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAAC  
GGGCTGCGGTCCCTGCGAGTGCTAACCCTCCATGGCAATGACATTTCCAGCGTTCTGAAGG  
CTCCTTCAACGACCTCACATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG  
ACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC  
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT  
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC  
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCTGCCCC

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## FIGURE 11B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTC  
TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA  
AACAAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC  
AGGTGAGCTATGCGACGAGGTGATTGACCACCTGTGTGCCTGAGCTGAACCTCTGTCAGCATG  
AGGCCAAGTGCATCCCCCTGGACAAAGGATTACGTGCGAGTGTGTCCCTGGCTACAGCGGG  
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCACAAAGTGCCGCCACGGGGCCCAGTG  
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCTTCTGTG  
AACACCCCCCACCCATGGTCCCTACTGCAGACCAGCCATGCGACCAGTACGAGTGCCAGAAC  
GGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGCTGCCACCAGGCTTCGCCGG  
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACCTGG  
CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC  
GGCATCCTTCTCTACAAAGGAGACAATGACCCCCTGGCACTGGAGCTGTACCAGGGCCACGT  
GCGGCTGGTCTATGACAGCCTGAGTTCCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA  
ATGATGGGCAGTTTTCACAGTGTGGAGCTGGTGCAGCTAAACCAGACCCTGAACCTAGTAGTG  
GACAAAGGAACCTCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG  
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGCACGG  
ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG  
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCACCAGGCTGCAAGTCTGCACCGT  
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
GCTGGACCGGCCCACTCTGCGACCAGGAGGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC  
CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG  
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCACCATG  
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC  
GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA  
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCTGGGGGCT  
GTGGGCCCCAGTGCTGCCAGCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGACAG  
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTT  
**CTAA**GCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC  
ATGTGGGACCCCCTGGTGAATTCAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA  
AGAGAATATTAAGTATATTGTAAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAA  
AAAAAA

## FIGURE 112

MAPGWAGVGAAVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGI PRN  
AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRLNKNKLQVL  
PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL  
TLNNNNISRILVTSFNHMPKIRTLRLHSNHLCDCHLAWLSDWLRQRRVTGQFTLCMAPVHL  
RGFNVADVQKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK  
GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL  
AQNPFCVCDCHLKWLDYLDQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEYRSRFS  
SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN  
LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV  
SNDTFAGLSSVRLLSLYDNRITTTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRR  
IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR  
ALPRGMPKDVTELYLEGNHILTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL  
SYNRLRCIPVHAFNGLRSLRVLTLHGNDISSVPEGSFNDLTSLSHLALGTNPLHDCSLRWL  
SEWVKAGYKEPGIARCSSPEPMADRLLLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT  
CTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR  
CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLCQHEAKCIP  
DKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV  
LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP  
QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS  
VELVTLNQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
HGCIEHVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC  
DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHISD  
QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ  
PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

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# **FIGURE 113**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA  
 GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
 CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG  
 GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG  
 GACAATTACTGGGGCTTCAGCCTTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA  
 CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
 ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC  
 TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
 GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG  
 AGTGGA AAAAAGGCTGTGAGGTTTCCTTAAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC  
 GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA  
 TTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT  
 TTAAATGTC

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## **FIGURE 114**

MKAAGILTTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCCEVS

**Signal peptide:**

amino acids 1-19

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## **FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFRLARRRKILFYCHFPDLLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTF LRSFS DKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

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# **FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACC**ATG**TTGGACTTCGCGATCTT  
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC  
AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT  
GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT  
CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC  
ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT  
CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT  
GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA  
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT  
ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG  
CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTCAC  
TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAAGTTCAGTCAACATATTTTCATTGACTC  
CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA  
GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCCTGTTACTCC  
AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTGCAACTGCCA  
AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT  
CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACTTTTTCCT  
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA  
GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA  
AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
AT**TAA**AATTTTATACATTTAAAATCATTGTAAATTGATTGAGGAAAACAACCATTTAAAAA  
AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC  
TTAA

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## **FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLVVSLSLGTVDVLKQHINPNKTSDFETMLKSLRLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLLLKLSEELLDKWLSTYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGTWVSEIGKGFLDGSLLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSSEEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVLCEVVRTAKLTPVSAQLQDIEGKIDRFIIPRETLLVLYALGVVL  
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

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# **FIGURE 119**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA  
 GACCGCCGCCCTTGTCCCCGAGGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
 CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT  
 ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG  
 TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA  
 GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
 GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT  
 TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAA  
 AAGAAACCCTT**CTGA**ATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
 CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCCTCGGAAACTGCTTC  
 TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
 GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA  
 ATTAAAAAAAAAAAAA

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## **FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT  
EMALFVTVFGLKKKPF

### **Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

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## **FIGURE 121**

TCCCGGACCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC  
AGCAGGCCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGCTAC  
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTTCACGGGTGC  
CCTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG  
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TG**AGGCC  
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAACCCCACTGTCTCCTTCTCCA  
ATAAAGATGTAGCTC

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## **FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

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## FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT  
 GACTCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
 ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
 CGGGTGCCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCAATCT  
 CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCCTTGGGCAGCCCCCAACCGCC  
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA  
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCC  
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCCGCCGGACCTC  
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTACCATAGTGATACCCCCTACTACCCATC  
 TGGG**TGA**CCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC  
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTCAGGCAGGGAGGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG  
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT  
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT  
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC  
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCTGTGTCTGAGCATG  
 GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCCACACTAAGGCC  
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG  
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCC  
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGA  
 GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGGAGGGGAGGGAAGTCTTGT  
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAGCTT  
 GCCCCGGGGCA



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## **FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR  
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY  
YPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACAGAGTGGGTGCAGGGGCCCCA  
GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG  
GACAAAGGTAAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
TGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGACCTAGCCGCTAG  
CATCTTCCCGAGCACCCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCCAGCGCCAGCC  
GGCTGCGGCTGCCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG  
GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
GCTCCTCTTCCCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG  
GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
CGATCAGATCCTGGTGAATGTGGTAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA  
GAAAAGGAATTTACAGTTTTCAGTTTTACGTGATTAAAGTCTACCAGAGCCAACTATCCAG  
GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC  
TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCCACGTTTTCTGGCTTTCTGGTG  
TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG  
AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG  
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG  
TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTTCATTTCCCTGGGATTACTGAATTAGT  
TACAGATGTGGAATTTTATTTGTTTAGTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
AACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTTTGGTTCTTGTA  
AAAACCTTGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA  
TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA  
GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT  
TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG  
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCCTCGAGGGAAATCTTATACTTTATTGC  
TCAACTTTAATTAAAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTTT  
TCCGTAGACATGACCACTTTATTAACTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA  
TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT  
CTTGCTTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA  
TTAATATATGTTAAAAAA

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## **FIGURE 126**

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSPATDSKGSSSSPLGI  
SVRAANSKVAFAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFFVAPRKGIIYSFSF  
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**  
amino acids 1-27

## FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
 GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC  
 TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA  
 TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC  
 TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
 GAAGAGTATAAACCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
 TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG  
 CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC  
 GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTTGATGGCTGTGAGAAGA  
 AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
 ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC  
 CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
 ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAA  
 ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG  
 GTGGAATTGAGAAAGAAATAAACTATGCAGATA

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**FIGURE 128**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658

&gt;&lt;subunit 1 of 1, 257 aa, 1 stop

&gt;&lt;MW: 28472, pI: 9.33, NX(S/T): 0

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN  
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF  
GIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKW  
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKN  
FLLYNQSR

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 129**

CGGCAACCAGCCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATG**TTGCTCTGGGCTTGCCCTTCT  
TGGTGCTCTTGGTGGCCTCGGTTCGAGAGCCATCTGGGGGTCTGGGGCCCAAGAACGTCTCGCAGAAAGACGCCG  
AGTTTGAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC  
GCAACAGGACAGAGGGCGTGCCTGTGTCTGTGAACGTCTGAACAAGCAGAAGGGGGCGCCGTGCTGTTTGTGG  
TCCGCCAGAAGGAGGCTGTGGTGTCTTCCAGGTGCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT  
ACCAAAAAGTGGAAACGAACCCGTGTGCAGCCCCACCAAGAATGAGTCGGAGATTAGTTCTTCTACGTGGATG  
TGTCCACCCTGTCAACAGTCAACACCACATACCAGCTCCGGGTGATCAAGGGCACCGCCAGAAAACCCGTGTCAGTGTGG  
GGGAGCAGTTAGCTTCAATACCACAGCAGCACAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT  
CGGTAATTGTCAAGGTGACCTCCAACAAGGCCTTCCCCTGCTCAGTCATCTCCATTAGGATGTGCTGTGTCTG  
TCTATGACCTGGACAACAACGTAGCCTTCATCGGCATGTACCAGACGATGACCAAGAAGGCGGCCATCACCGTAC  
AGCGCAAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGGCT  
CCCTGCCTTTCTACCCCTTCGCAGAAGATGAACCGGTGATCAAGGGCACCGCCAGAAAACCCGTGTCAGTGTGG  
TGTCTCAAGCAGTCAGTCTGAGGCATACGTGAGTGGGATGCTCTTTTGCCTGGGTATATTTCTCTCCTTTTACC  
TGCTGACCGTCTCCTGGCCTGTGAGGAACTGGAGGCAGAAGAAGACCCCTGCTGGTGGCCATTGACCGAG  
CCTGCCCAGAAAGCGGTACCCCTCGAGTCTGGCTGATTCTTTTCTGGCAGTTCCCTTATGAGGGTTACAACT  
ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG  
GTTACCAAGGGCCGCTCCTTTGAACCTGTAGGTACTCGGCCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG  
ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTATTTCGCACCAAGCAATACCTCTATGTGGGTGAC  
TGGCACGGAAGGACAAGCGTGTCTGCGGAAAAAGTACCAGATCTACTTCTGGAACATTGCCACCATTGCTGTCT  
TCTATGCCCTTCTGTGGTGCAGCTGGTGATCACCTACCAGACGGTGGTGAATGTACAGGGGAATCAGGACATCT  
GCTACTACAACCTTCTCTGCGCCACCCACTGGGCAATCTCAGCGCCTTCAACAACATCCTCAGCAACCTGGGGT  
ACATCCTGCTGGGGCTGCTTTTCTGCTCATCTCCTGCAACGGGAGATCAACCACAACCGGGCCCTGCTGCGCA  
ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCACAGCCCTGATGA  
TGGAGGGGCTGCTCAGTGCTTGTATCATGTGTGCCCAACTATAACCAATTTCCAGTTTGACACATCGTTTCATGT  
ACATGATCGCCGGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCCGGACATCAACGCCAGCGCCTACAGTG  
CCTACGCCTGCCTGGCCATTGTCTATCTTCTCTGTGCTGGGCGTGGTCTTTTGGCAAAGGGGAACACGGCGTTCT  
GGATCGTCTTCTCCATCATTACATCATCGCCACCCTGCTCCTCAGCACGCAGCTCTATTACATGGGCCGGTGGA  
AACTGGACTCGGGGATCTTCCGCCGCATCCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC  
TCTACGTGGACCGCATGGTGTCTGCTGGTTCATGGGCAACGTTCATCAACTGGTCTGCTGGCTGCCTATGGGCTTATCA  
TGCGCCCCAATGATTTTCGCTTCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAGAGTCGAGGGAGCACA  
TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTTGCACCTCCGTGGTCT  
GGGCTTTCGCGCTCTTCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAGAGTCGAGGGAGCACA  
ACCGGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACATCTGGCACTTCTCTCCTCCATCGCCATGTTTCG  
GGTCTTCTGCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGCAGCGGGACAAGATCTATGTCTTCT**TAGC**  
AGGAGCTGGGCCCTTCGCTTCACTCAAGGGGCCCTGAGCTCCTTTGTGTATAGACCGGTCACTCTGTCTGTGCT  
GTGGGGATGAGTCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT  
GGGACAGCCATGGGGTGGCATGGAACCTTGCACTGCCCTCTGCCGAGGAGCAGGCCTGCTCCCTGGAACCCCC  
AGATGTTGGCCAAATTGCTGCTTCTTCTCAGTGTTGGGGCCTTCATGGGCCCTGTCTTTGGCTCTCCATTT  
GTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCTCCCCATTTTCATGCCTTGCAATTTTGGCCGCTCCTCCTCCC  
ACAATGCCCCAGCCTGGGACCTAAGGCCTCTTTTCTCTCCATACTCCCACTCCAGGGCCTAGTCTGGGGCCTGA  
ATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCACTGCCATTCCAGTCAGCC  
AGGATGGATGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGCCAGACTTTTGGTGCTAAGGCCTGCAAGGGG  
CCTGGGGCAGTGCATTTCTTCTTCCCTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAATT  
TGAGAACCGCCTTCTGATTCAAGAGGCTGAATTCAGAGGTACCTCTTCATCCCATCAGCTCCAGACTGATGCC  
AGCACCAGGACTGGAGGGAGAAGCGCCTCACCCCTTCCCTTCTTCTTCCAGGCCCTTAGTCTTGCCAAACCCCC  
AGCTGGTGGCCTTTTCAGTGCCATTGACACTGCCCAAGAATGTCCAGGGGCAAAGGAGGGATGATACAGAGTTTCAG  
CCCGTTCTGCCTCCACAGCTGTGGGCACCCAGTGCCCTACCTTAGAAAGGGGCTTCAGGAAGGGATGTGCTGTTT  
CCCTCTACGTGCCAGTCTTAGCCTCGCTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTTCAGGCA  
AGTTCTGTGTTAGTCATGCACACACATACCTATGAAACCTTGGAGTTTACAAAGAATTGCCCCAGCTCTGGGCAC  
CCTGGCCACCCTGGTCTTGGATCCCCTTCTGTCACCTGGTCCACCCAGATGCTGAGGATGGGGGAGCTCAGG  
CGGGGCTCTGCTTTGGGGATGGGAATGTGTTTTCTCCAAACTGTGTTTTATAGCTCTGCTTGAAGGGCTGGG  
AGATGAGGTGGGTCTGGATCTTTTCTCAGAGCGTCTCCATGCTATGGTGCATTTCCGTTTTCTATGAATGAATT  
TGCAATCAATAAACAACCAGACTCAAAAAAAAAAAAAA

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## **FIGURE 130**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659

><subunit 1 of 1, 832 aa, 1 stop

><MW: 94454, pI: 6.94, NX(S/T): 12

MFALGLPFLVLLVASVESHGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT  
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE  
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTEGEQFSFNTTAAQPQYFKYEFPEGVDSVI  
VKVTSNKAFFPCSVISIQDVLCPYDLDNNAVFIGMYQTMKKAAITVQRKDFPSNSFYVVVV  
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTL SVLV SQAVTSEAYVSGMLFCLGIFLSFYLL  
TVLLACWENWRQKKKTLLVAIDRACPESGHPRLADSFPGSSPYEGYNYGSFENVSGSTDGL  
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL  
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVNVTGNQDICYNFLCAHPLGN  
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGFLFYAMGTALM  
MEGLLSACYHVCPTYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS  
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYIMGRWKLDSGIFRRILHVLYTDCIRQCSG  
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI  
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDFDHDHDIWHFLSSIA  
MFGSFLVLLTLDDDLDTVQRDKIYVF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-18

#### **Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

#### **Leucine zipper pattern.**

amino acids 497-518

#### **N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

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**FIGURE 131**

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGCTTGCCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCCTG  
 ACC**ATG**GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACC  
 TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA  
 GGCAAGGCCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG  
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG  
 CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC  
 CTTCTCTTCCTTGAGGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT  
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCCTATACCCGCACCACATGGCCAGGTACACTGGAGTGGGGGTGATGT  
 GCACTATCACCTGGAGAGCCATCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
 AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA  
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGACTAGACTGTCAGCAGAGGATGCAGATGCCCCGGCTCCCCAATTCC  
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA  
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA  
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT  
 GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGAT  
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA  
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGAAGTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGGCCAGTGTCCCCATCAGTGCCCC  
 AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCT  
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCTCCGGGGAGGTGCACACC  
 GCCAGTCCCTGCAGGGCGCCCAGCCTGGGGACACCTACACGGTGTCTTGTGGAGGGCCAGGA  
 TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG  
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC  
 TTCACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC  
 CCATGCCTACCTACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG  
 TGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGTGCTGCAAC  
 GTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCACGAAGCTGTGCGC  
 AGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCCTCATCCTCATTTTACACC  
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG  
 ACTGTCT**TGA**ATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC  
 TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTTTGCCCAATAATAAAGCCCCA  
 GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG



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## **FIGURE 132**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDFMFQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSIESTWVSLEPIHLAE  
NLKVLYPHMAQVHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN  
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH  
VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE  
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRLMDFAIERGDTE  
GTFGLDWEPSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV  
MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA  
QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHII PVVVSNAQMWQLLV RVIVCRCNV  
EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

### **Signal peptide:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 762-784

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**FIGURE 133**

CCGGGGAC**ATG**AGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT  
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCACTCTGCAGGCATTTAAATCCTTCCTG  
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTAGACAATGA  
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT  
 CAGCACTGGGAAAGGCGTGAGGCGGCCGCGCTTTGGCTGAATGCAGGCATCCATTCCCGAG  
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG  
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTGCCTGTGGCCAATCC  
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC  
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG  
 GGAGCCAGCGACAACCCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGA  
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC  
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC  
 GAGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGGGCACTGA  
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
 CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC  
 TTCCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGACAACCTCTAC**TAG**GGCGATGGCTCTGCTCTGTCTACATTTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG  
 TCAGAGCCCTCTGGGTTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
 CGTGTGTCCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCCTG  
 CTGTTTTTGATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC  
 AGCATCACCCCTTCCCTGGGTGGCATGTCTCTCTCTACCTCATTTTTTAGAACCAAAGAACATC  
 TGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT  
 GTGGGAGACACCACCTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTT  
 TCGCAGTCTTCCCTGGAAAATATTTTCCCTTTGAGCAGCAAATCTTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTTGCC  
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCAACCTCTGCCTCCTGGGTTCAAGCA  
 ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA  
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA  
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG  
 TGCCGGGCGCGTCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCAC  
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCACTGTG  
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTGCAGGATGGTGAAATTATCCCCATCTGTCCTAATGGGCTTACCTCCT  
 CTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTTAAATCACTCAT  
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTGTATCCTGTGTT  
 TCCTTGTCTGGTTTTG  
 TCTGTCTATTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT  
 GCCTCTTGTTTTCATTTACCTCAGCACGTACCATCTGTCTTTTGTGTTGTTGTTTGTGTTT  
 TTGTTTTTTTGTCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA  
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAA

**Signal peptide:**  
amino acids 1-16

[illegible]

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## **FIGURE 136**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
 TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP  
 SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK  
 VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
 GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
 SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
 KFIVRSKDGPSYFTVSNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

**FIGURE 137**

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## **FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI  
 SGSSVTSNGVSIIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE  
 SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
 TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT  
 SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS  
 GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
 NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST  
 ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV  
 SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHHPGLNHGLGP  
 GPGGNHGHAPHRPRWSPNWFWRPVS SIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

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## **FIGURE 139**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
 CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
 CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC  
 ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
 AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAAACAACG  
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC  
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
 TGCAGAAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
 GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
 TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC  
 ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG  
 GGATTTGTGAATAAACTTGATACACCA



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## **FIGURE 140**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGLSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG  
 REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHG VNNAAG  
 QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN  
 AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

[illegible]

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**FIGURE 142**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

&gt;&lt;subunit 1 of 1, 837 aa, 1 stop

&gt;&lt;MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF  
EAEHISNYTALLLSRDGRTLTVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG  
KDPQRDCQNYIKILLPLSGSHLFTCGTAAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCF  
FDPNFKSTALVVDGELYTGTVSSSQGNDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE  
SLGSLQGDDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC  
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG  
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFLMDGQVR  
SRMLLLQPQARYQQRVAVHRVPGLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIEELQIFSSGQ  
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQP  
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCQVQFQPNNTVNTLACPLLSNLATR  
LWLRNGAPVNASASCHVLPTGDLLLVTGQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ  
TDEGGSVPVPIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM  
KVFLKQGECAVHPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR  
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

CTAAGCCGAGGAGTGTGCAGCTGCGGCGGCGGCGCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCA  
GCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCCGCCGTCTGCGCGTCC  
TGCCGGCCCCCGCTCCCCGCGCGAGCGGGAGGAGCGCCGCCACCTCGCGCCCGAGCCGCCGCTAGCGCGCGC  
CGGGCAGTGGTCCCCCTTAAAGGCGCAGGCGCGGCGGCGGGGCGGGGTGTGCGGAACAAAGCGCCGGCGCGGG  
CCTGCGGGCGGCTCGGGGCGCGATGGGCGCGGCGGGCGGCGGCGCGCGCGCTGCCCGGGCGGGCTCG  
CGGCGCTAGGGCGGGCTGGCCTCCGTGGCGGGGGGACGGGCTGAGGGCGCGCGAGCCTGCGGCGCGCGCGC  
GGCGGCGGCGGCGGCCCGGCGGGCGGAGCGGCGCGGGC**ATG**GCGCGCGCGCGCGCGCGCTGGCTCAGCGTGC  
TGCTCGGGCTCGTCTTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG  
GCCACGCGCGCCGCGCCAGCGCCCGAGGGTGGCGGTCCGGGACAGGCGGCGGCTTCCAGGCCGGCGGGGCGCGCG  
CGGATGCGCGCGGGGCGAGCTTGGCCGCCCGGCTCGGACCCAGATGGCGGCGCGCGCGCAGGAACCTTCTCT  
TCGTGGGAGTCATGACCGCCAGAAATACCTGACAGCTCGGGCGGTGGCGGCTACAGAACATGGTCCAAGCAA  
TTCCTGGGAAAGTTTCACTTCTTCTCAAGTAGGGGTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGG  
GTGTGGACGACTCCTACCCGCCCCAGAAGAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA  
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAAGTCTTCTGAGGAGTT  
TGAACAGCAGCGAGCGCCCTCTTCTTGGGCGAGACAGGCTGGGACACCAGGAAGAAATGGGAAAAGTGGCCCTGG  
AGCCTGGTGAGAAGTCTGCTATGGGGGGCTGGCGGTGATCATGAGCGGGAGGTGCTTCCGGAAGTGGTGCCGCG  
ACATTGGCAAGTGTCTCCGGGAGATGTACACCCAGTGAAGACGTGGAGGTGGGAAGGTGTGTCCGAGGTTTG  
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCGAGCTTTTTTATGAGAATTACGAGCAGAACAAAAAGGGGT  
ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATCACATTACCCCCAACAAAAACCCACCCTACCAGT  
ACAGGCTCCACAGTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAAA  
TTGTCTCTGATGAGCAATACAGCAACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA  
TGAGGTTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATTGGAGTTTCTGACTGGAAATACTGTATTCCGCGC  
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGGAAGCCTTGGACGACATTGTCTGATGAGGTCA  
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATTGACTTCAAAGAGATCCAGTACGGCTACCGCC  
GGGTGAACCCCATGTATGGGGCTGAGTACATCTGGACCTGCTGCTTCTGTACAAAAGCACAAGGGAAGAAAA  
TGACGGTCCCTGTGAGGAGGCGAGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC  
TGGATGCACAAGAGTTTGGCCAAAGAAATCAATCAGGAATCTGGATCTTGTCTTCTTCAAATCCCTGAAGA  
AGCTCGTCCCCTTTTCACTCCCTGGGTCGAAGAGTGAGCACAAGAACCCAAAGATAAAAAGATAAAACATACTGA  
TTCCTTTGTCTGGGCGTTTTCGACATGTTTGTGAGATTTATGGGAAACTTTGAGAAGACGTGTCTTATCCCCAATC  
AGAAGCTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCCTGACAAGGCCAACAAAGTTGAAGTATGA  
GAGATTACCGCATTAAGTACACCTAAAGCCGACATCGAGATTTTGCTGTGTCTGGAGAGTTTTCAAGAGCCCTGG  
CCCTGGAAGTAGGATCTCCAGTTTAAACAATGAATCTTGTCTCTTCTTGCAGCTCGACCTCGTGTTTTACTA  
CAGAATTCCTTTCAGCGATGTGCGAGCAAAATACAGTTCTGGGCAACAATAATATATTTTCCAATCATCTTCAGCCAGT  
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCTTTACTCAGAAAAGTGGCTTCT  
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA  
TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC  
AGGAAGTAGGAGTAGTCCAGTCCACCTCCTGCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT  
GCTTGGGGTCCAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA  
GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCT**TAAT**GTCCAGCTTTGCTGGAAAAGACGTTTT  
TAATTATCTAATTTATTTTTTCAAAAATTTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC  
AAGTGGTTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTCTGAACAAGAAGGTGATCAGTGTGTGCTTTGAA  
CACATCTTCTTGCTGAACATTATGTAGCAGACAGCTGCTTAACTTTGACTTGAAATGTACCTGATGAACAAAAGT  
TTTTAAAAAATGTTTTCTTTTGGAGACCTTTGCTCCAGTCTTATGGCAGAAAACGTTGACATTTCTGCAAAGTAT  
TATTGTAACAAAAGCTGTAACCTGTTAAATGTTCTGTTGTGATTGTTAACTTCCAGATTTACCTCTTCTGTTGT  
GTTTTGTTTTTTTTTTTTTACAATTGTTTTAAAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA  
GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC  
CACGTAGGTTTTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG  
CAGTGGCGCAATCTTGGCTCACTTTTAACTCCACTTCCCTGGTTCAGGCAATTTCCCTTGCCTTTGCCCTCCCGAGT  
AGCTGGGATTACAGGCACACACCACCGCCAGNATGTTTTTTTTGATTTTTTAGTAGAGACGGGTTTCCACAT  
GCAAGCCAGCTGGCCACGTAGGTTTTAAAGCAAGGGGCGTGAAGAAGGCAGTGAAGGTATGTGGCTGTCTCTCG  
TGGTAGTTTATTGCGCCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTTGGCATTCTTCTTCTTGACCCCTT  
CTCTTTAAAGGGTAAAATATTAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT  
GAAACATACACACATACACCCTAATCAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCTTTCATCCTGTCTG  
TGTTATGTGGGTGGAGATGTTTTTCACTCTTCACTACTGTTTTGTTTTTATCTTTTGTATCTGAAATACCTTTAA  
TTTTTTAATATCTGTTGTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATGATGTATCGG  
GAGTGTGTTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCTTTTTGGAACGCTTTTTTCCCTCC

## **FIGURE 143B**

TTAATTTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTGGTGCTCATGTGTTTTGGG  
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT  
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG  
CCTGATGCTCATTTGGAAAAATAAACCAGTGAACAATATTTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT  
ATTCCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAAA

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## FIGURE 144

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR  
 GDARGAQLWPPGSDPDGGPRDRNFLFVGVMATAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEG  
 SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRAADDVYIKGDRLENFLR  
 SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYT  
 THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP  
 YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFQPRQREE  
 ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
 GYRRVNP MYGA EYILD LLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
 INQESGSLSFSLNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFECTC  
 LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ  
 FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
 QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDDVDFNKVVQAGLKTFRSQEVGVVH  
 VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

### Signal peptide:

amino acids 1-23

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# **FIGURE 145**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
ACGGACGACGCCT**ATGA**AAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG  
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC  
TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA  
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA  
ACTTTCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAAACACACGGAAAGTACCCC  
ATTCTGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG  
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG  
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCAC  
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAAT  
GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA  
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC  
TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA  
GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC  
TAGATCTAACTCTATGAATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG  
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
AAAGTTTAT**TAA**ACAATAATATAAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA  
TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTTCGTAATTTCAAAGTTGTAT  
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA  
ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGGTTCAGGAAAAAA

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## FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPK  
 HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTTFPTGGFTPEIGKKKHTESTPFWSI  
 KPNNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTTLDK  
 STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP  
 AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQQLPVGRTSNKIDDIETVINMLCNSRSKL  
 YEYLDIKCVPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19



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**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACA  
 GGAATATCC**ATGG**CTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA  
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
 CCTGCTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAG  
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA  
 GTATCGAGGGAGAAGTGAAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC  
 TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTTTAC  
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT  
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC  
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA  
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT  
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG  
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT  
 GCCCTGTGTGGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA  
 GGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG  
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA  
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA  
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC  
 AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG  
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC  
 ATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC  
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC  
 CTGCTGACATGTCAGTTTGAAGGCTTGTGAGACCCTATATCCAGCATGCGATGTATGACGA  
 GGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTTGGGGAT**TGAG**ACAGAGAAGACCCTG  
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC  
 CCCAGCTTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCCTCTCCTTTAGGGAGC  
 TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT  
 TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA  
 CATTAGGTTTAGTTTGTGAAAACCTCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
 CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTTGCCTCACAGGTGAAGATTAAAGAGA  
 CAACGAATGTGAATCATGCTTGCAGGTTTGAAGGACAGTGTTTGTCTAATGATGTGTTTTTA  
 TATTATACATTTTCCCACCATAAACTCTGTTTGTCTTATTTCCACATTAATTTACTTTTCTCTA  
 TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG  
 GAGGTAGGATTTTCTACTGATTCTATAAGCCCAGCATTACCTGATACCAAACCAGGCAAAG  
 AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAA  
 TTCTAAATAAAATTTTAACAAATTAACTAAACAATATATTTAAAGATGATATATACTACT  
 CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAGTGTAATT  
 CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

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## FIGURE 148

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop .

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
 VHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSQIYDEE  
 ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY  
 SLYDVEISIIIVQENAGSILCSIHLEQSHVESKVLIGETFFQSPWRLASILLGLLCGALC  
 GVVMGMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT  
 HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDVGKNNVTLS  
 PNNGYWVLRLLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT  
 CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

### Signal peptide:

amino acids 1-17

### Transmembrane domains:

amino acids 131-150, 235-259

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## FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA  
GGAAAAGAGTTTGTGGGAACCCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC  
CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAA  
TTACTATAGCACATTGTCAATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGGCTT  
CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA  
TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG  
ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCTAAAGTA  
GATCCTCACTCAGTTAAAATTAAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG  
AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA  
GAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG  
GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT  
CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA  
TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA  
ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCT  
TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
AGAAGGAAAAACAGATGCATGCCAGGGTGAAGTCTGGAGGACCACTGGTTAGTTCAGATGCTA  
GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG  
CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA  
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT  
TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
TGTTTGCTTGATGCATGTATTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATA  
ATACAATATTACATTACAGCCTGTATTTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAC  
TTGTTGACATAAATTTGTAATGCATATATAACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC  
AGCTCCTCTCATTTTCAAGCAATATCCATTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATA  
TAAGAAGAAAAAAATCCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT  
GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC  
ACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA  
TCCTTATTTTCAATTTCCAAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG  
ACCTATAATAATTATACAAACTTCATGCAATGTACTTGTCTAAGCAAATTAAAGCAAATAT  
TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

## **FIGURE 150**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSVPYPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

### **Transmembrane domain:**

amino acids 21-40 (type II)

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## FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
 CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG  
 CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGC  
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCCTGCCTGTGCCC  
 AGGACTCTCCAGCCCCGCCAGCCGCCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG  
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCCCTCCACTACTGG  
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGGCCCCCGCTGAACGCTACGGTCCG  
 CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGGCATTTATGTCGTTTGCGTAGTGGCCGCTA  
 ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC  
 CCTGCCTTCGGGCCTTGACAGCCGCCTTGCGGTGCCGCCCAACCCCCGCACTCTGGTCCACGC  
 GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
 GCCTGCGCGATCGCTGGGGCTGCCCCGCGCCGAGCCGCCGCCCGAGCCGCAGGGGGCGCTC**TGA**  
 AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG  
 GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG  
 GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT  
 GGCGCTTTGTTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTTTA  
 AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAAA

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
```

```
><subunit 1 of 1, 238 aa, 1 stop
```

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE  
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA  
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRPQAGGEGLEGADIPAFGPCSRL  
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLRDWRWGCPRRAAARAAGAL

### Important features of the protein:

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

N-glycosylation site.

amino acids 132-135

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## FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
 CTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGG  
 CCCAGCGCCGACGATCGCTGCCGTTTTGCCCCTGGGAGTAGGATGTGGTGAAAGGATGGGGC  
 TTCTCCCTTACGGGGCTCACAA**ATG**GCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT  
 CTACGCCCTCAATCTGCTCTTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA  
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC  
 ATTTTGACTTACTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCAT  
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCAATGGTACT  
 TTGGAAGTTTGCTTGTCATTTTCTGTGTAGAAGTGGCTTGTGGCGTTTGACATATGAACAG  
 GAACTTATGGTTCAGTACAATGGTCAGATATGGTCACCTTGAAAGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGAATTTTTTTTCAGAGAGAGTTTAAGT  
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAT  
 TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA  
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAAACAACCTGC  
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTC  
 CTTGAAGAATGACAACCTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCC  
 TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG  
 GAGTTA**TAAAA**AGAAATGTCACAGAAGAAAACCACAACTTGTTTTATTGGACTTGTGAATT  
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA  
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC  
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTTC  
 CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT  
 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA  
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTTC  
 AATATTGGTGACTACCTAAATGTGATTTTTTGCTGGTTACTAAAATATTCTTACCCTTAAAA  
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA  
 TCTGTATAATTACAGTCGATTTTCAGTTCCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA  
 ATTTGTCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT  
 CCTGGGCTTATATTACACATATACTGTTATTTAAATACTTAACCACTAATTTTTGAAAATTA  
 CCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAA  
 GAAAATTTGCACATAACTTAGTTGATTACAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATG  
 AAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA  
 GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTCTTTTTTCTCCAGAAAAAT  
 GCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTA  
 ATATACTGTGGCAAATTACACAGATTATTAAATTTTTTACAAGAGTATAGTATATTTATTT  
 GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTCTCAGAATATGGAA  
 AGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA





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# FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC  
TGCACCTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA  
CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
ACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC  
CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT  
CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGG  
TGATTCTGGATAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG  
CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
ACTCGGCCACAGGGAACTGGTTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAG  
ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA  
TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTC  
TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCCGT  
GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGA  
CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCAGCCCACT  
GCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC  
AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCCAA  
AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTTTCTCAGGCACAGTCAGGC  
CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCCACTCTGGATCATTGGA  
TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA  
GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGGAAGTCACCGAGAAGA  
TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC  
CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG  
GGGCCCAGACCCCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTG  
CCCTGCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC  
CTCTGCCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCC  
TCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC  
AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA  
GGAACTTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG  
CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA  
CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
ACCTACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT  
CTGGCAAAAAAAAAAAAA

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## **FIGURE 156**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPPIIIALLSLASIIIVVVLIKVILDKYYF  
 LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAAVAVRLSKDRSTLQVLDSATGNWF  
 SACFDNFTEALAETACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPGCLSGSLVSL  
 HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWLTAAHCFRKHTDV  
 FNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD  
 EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE  
 GGVDTQCQDSSGGLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

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## **FIGURE 158**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ  
 DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQC  
 FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA  
 VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAAIPSTQVVYFFFE  
 ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL  
 PADSPAPHIYAVFTSQWQVGGRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET  
 NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM  
 YLGT TTGSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN  
 CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP  
 QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAPVEASSTVYNGSLLLIVQDGVGG  
 LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP  
 HFVTVTVLFLVLVSGALIIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT  
 SASDVDADNNCLGTEVA

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704

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## FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG  
TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCGTGCTC  
TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG  
GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGG  
TGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC  
ATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAAGTTTCGACATGGTGATA  
GTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC  
CATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT  
CAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG  
ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA  
GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
GGTTCATTAACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT  
GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGGAGAACTTCATTGC  
CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA  
ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG  
AAGTGTGAGTGTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGA  
CTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCG  
GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT  
GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTT  
AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
ACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAG  
CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA  
TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGC  
TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT  
GGGGCCAGAAAGGTGAAGGAGACAT**TAA**GGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG  
GCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC  
TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC  
TAATTTTGTCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT  
CTTGTCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
GACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCTCTCCGAA  
TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC  
TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAAGTTTCTGTTT  
TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGC  
CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT  
TCTTGGCTGAGCAGGCATGGAGACTGTAGTTTCCAGATTTCTTGAAAAATAAAAGTTTACA  
GCGTTATCTCTCCCCAACCTCACTAA

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## **FIGURE 160**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKPKFVAILSTSFSGSLEFGLPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP EIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 483-504

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## FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTT  
CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT  
GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA  
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT  
GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCCAGCGAGCCTAGAGAGGGC  
AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGGCAGA  
AGACCGGGGGCACTTGTGGGTTGCAGAGCCCCCTCAGCC**ATG**TTGGGAGCCAAGCCCACTGGC  
TACCAGGTCCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC  
GGGTGGGCCCAGGAGGGGTCCAGAGCCCGTCCCTGCTGGAGGGGGAGTGCTGGTGCTTCTGTGA  
GCCTGGCCGAGCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC  
GAGTGGCATTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC  
ACCAGTGGGGCCATCTACTTCGACCAGGTCTTGGTGAACGAGGGCGGTGGCTTTGACCGGGC  
CTCTGGCTCCTTCGTAGCCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG  
TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTATCTCAGCC  
TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGA  
CCCTGGGGACCGAGTGCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACT  
CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCT**AG**AGGACCCAAGTCTTTCAAGCACAAGAAT  
CCAGCCCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG  
ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAA  
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTTAA  
CTCCCAGCCACCTGCTGCATCTGTTCCCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGA  
AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCCCCCACCCCAAGTTTAA  
GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCCAG  
ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCCTGTGAGGAAAGCCAGCATCACGGATC  
TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC  
AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG  
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
GGCTGTCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG  
GGTGAGTGTGTTTGTCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
ACCATGGAAAACATCGATAACCATGCATCCTCTTGGCTTGGCCACCTCCTGAAACTGCTCCAC  
CTTTGAAGTTTGAACTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCCCTCCCAGCTCTC  
TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTTTCTCCTGAT  
CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCTTATTACCTGGGATTCCATGATTCAATCCTT  
CAGACCCCTCTCCTGCCAGTATGCTAAACCCCTCCCTCTCTCTTTCTTATCCCGCTGTCCCAT  
GGCCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCAGTGAGACACTAT  
AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGGTA  
TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAAATTAAAA

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## **FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECCLVVCEPGRAAAGGPGGA  
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY  
SFRFHVVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG  
NLLGGWKYSSFSGFLIFPL

**Signal peptide:**

amino acids 1-32



[illegible]

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## **FIGURE 164**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS  
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIYVLYFTWLVDWNTPKKGRRS  
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP  
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM  
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA  
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK  
HKTKFGLPETEVLEVN

### **Important features of the protein:**

#### **Transmembrane domain:**

amino acids 76-97

#### **N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

#### **N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

# FIGURE 165

GGGCGGCGGGATGGGGGCCGGGGCGGGCGCGCGCGACTCGCTGAGGCCCCGACGCAGGGCCGGGCCGGGCCCA  
GGGCCGAGGAGCGCGGGCGGCCAGAGCGGGGCCGCGGAGGCGACGCCGGGGACGCCCCGCGACGAGCAGGTGGCG  
GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGA  
CGGCTGTCCTCAGCGAGGGGGCCGTGCACCCGCTCCTGAGCAGCGCCATGGGCTGCTGGCCTTCTGAAGACCCA  
GTTTCGTGCTGCACCTGCTGGTCGGCTTTGTCTTCGTGGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC  
GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA  
ACTGGTCATGCTGCTGGAGTGGTGGTCTGTCACGGAGTGACACTGTTACGGACCAGGCCACGGTAGAGCGCTT  
TGGAAGGAGCACGCAGTCATCATCTCAACCACAACCTTCGAGATCGACTTCTCTGTGGGTGGACCATGTGTGA  
GCGCTTCGGAGTGCTGGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC  
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG  
GCGCCTGTGCGACTACCCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACGCGCTTACGGAGACCAAGCA  
CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG  
CTTACACACCGCAGTCAAGTGCCTCCGGGGGACAGTCGCAGCTGTCTATGATGTAACCCTGAACTTCAGAGGAAA  
CAAGAACCCGTCCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCTCT  
GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACGCGCTCCA  
GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCGAGGCGGTGGACCCCTCTGAA  
CTTCTGTCTGCTGGGCCACCATTTCTCTGTCTCCCTCTTCAGTTTTGTCTTGGGCGTCTTTGCCAGCGGATCACC  
TCTCCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT  
TGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT  
CAGTCTCAAAAAAAAAAAAAAAAAACAAAAAACCCAGAAATTTCTGGAGTTGAACTGTGTAGTTACTGACATGAAAA  
ATTCAGTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT  
TTTACGGCTAATGAAAAAGAATGAAGGAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA  
CATATGCATGATGAGAGTCCAGAAAGGAGAGAGAGAAAGGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA  
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCA  
AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTTG  
ATCAGATTAACAGCTCATTTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA  
AACCTTCAACTGTAATTATTGGACTTTTGTAGTCTTAGATGGTCTGACCTCTTTGTCTTCAGGGACAGTTTTTCA  
ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGACCTGTAGGAAGGCCTGTCTTTAGGCCGGGCACAGTGGC  
TTACACCTGTAATCCCAGCACTTTGGGAGGCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACCTCCT  
GAGTTCAGGTGATCTGCCCCCTCAGCCTCCCAAAGTGTTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA  
ATTTCTTTTTTAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCCTGTGATCCCAAGTAGCTTGGATTGTA  
AACATGCACCACCATGCCTGGCTAATTTTTGTATTTTGTAGTAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCT  
GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA  
GCATCTTGTGATGTGCTTATTGGCCATTTGTATATCTTCTATCTTCTTTGGGGAAATGTCTGTTCAAGTCCTTTG  
CCTTTTTTAAATTTTTTATTATTTATTTATTTATTTTGTAGACAGGGTCTTGTCTGTTGCCAGGCTGGAGTA  
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT  
AGCTGTATTTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA  
TGCCAGGCTGGTCTTGAACCTCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGCTGGGATTACAGA  
CATGAGCCACTGCACCTGGCAAACCTCCCAAATTC AACACACACACACAAAAACCACCTGATTCAAATGGGCA  
GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG  
CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

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## **FIGURE 166**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFFVVSGLVINQVQLCTLALWPVSKQLYRRRLNCRLAYSLWSQLV  
 MLEWWSCTECTLFDTQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSSKVLAKK  
 ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR  
 VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAYVDVTLNFRGNKNPSLLGILYGGK  
 YEADMVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN  
 FLSWATILLSPLFSFVLGVFASGSPLLLTLTFLGFVGAASFGVRRRLIGESLEPGRWRLQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169

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## FIGURE 167

GATATTCTTTATTTTAAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCA  
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT  
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG  
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG  
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCTTGGGATCTGCCTATACCTTCTT  
TTCTCTAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA  
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT  
ACATGTGGTGTCTCTTGTCTGCTTCCT**GTA**ATGTGGTATGCCATGGGGTCTTTGCACAAGCCT  
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC  
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
CTTGTTTAAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCCAGCTCTGAGC  
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT  
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA  
GATGGTGTAGGGCCCAGCATTGTAAATTACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
TGCAGGTCCTGATTCAGTAGGCCAGGTGGGCATCTCTAACAACTCCCACGTGATGCTGA  
TGCTGGTCCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
TCAAGACTAGCCTGGCCAACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTG  
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

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## **FIGURE 168**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRHIHLCVCF SFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR  
EGKINFYTN GDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS  
GPCPPGQLHCTCGVLLSFL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

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## FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA  
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC  
AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
ATTAAATCTGTTTTTTGTTCTCTTGTAAC TAGCCTTTACCTTCCTAACACAGAGGATCTGT  
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC  
ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
ACCAACTGTCTCACGTCTGGAGGCCTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGA  
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGA**CAAGCCCGAAGATTT  
CATAGGCGATGGCTCCCCTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCAT  
CTAACCTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG  
AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
TATGTGACAGGACTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA  
GGGAAGGAACTTGTGCCAAATTATGGGTCAGAAAAGATGGAGGTGTTGGGTATCACAAGGC  
ATCGAGTCTCCTGCATTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG  
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG  
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCCTCCTTCCCTC  
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG  
GCTCAGTGTTGGCCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG  
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAAATCCCCAGGCAAAGGACTGTGTGGCT  
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
TCAAATGATCTCCAAGGGCCCTTATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAA  
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG  
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG  
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT  
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
AAAAATAAAAAAAGAATTATGGTTATTTGTAA

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## **FIGURE 170**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA

SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15



## FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
 CCGCCGCCTCCTGCCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCCGCCGCGCT  
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT  
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCCTGCTTCCCCCGAGGACAGCCGCTGTGG  
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
 CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC  
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC  
 CTGGCCCTGGCCCTGGCGCTGCCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA  
 GCCCCCGGAGCTGGGACGGCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC  
 GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC  
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC  
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
 GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  
**CTAG**GGCTGGCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC  
 CCTGAGTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 172**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282

><subunit 1 of 1, 262 aa, 1 stop

><MW: 28809, pI: 8.80, NX(S/T): 1

MTQVPVRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS  
MREHPALRSLRLLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSAALALAL  
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDELLAAGEAGTFDVAVVDA  
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS  
LLPLGDGLTLAFKI

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domains:**

amino acids 8-30, 109-130

#### **N-glycosylation site.**

amino acids 190-193

#### **Tyrosine kinase phosphorylation site.**

amino acids 238-246

#### **N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

#### **Amidation sites.**

amino acids 31-34, 39-42

CCGCGCCGCGCAGCCGCTACCGCCGCTGCAGCCGCTTTCCGCGGCCTGGGCCTCTCGCCGTCA  
GC**ATG**CCACACGCCTTCAAGCCCGGGGACTTGGTGTTTCGCTAAGATGAAGGGCTACCCCTCAC  
TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCAACAAGTACCC  
CATCTTTTTCTTTGGCACACACGAAACAGCCTTCCTGGGACCCAAGGACCTGTTCCCTTACG  
ACAAATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGG  
GAGATCCAGAACAACCCCCACGCCAGCTACAGCGCCCCCTCCGCCAGTGAGCTCCTCCGACAG  
CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG  
GGGTTCATGGCCGTCACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA  
GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGATGTC  
GGTCTCGAAACGAGCCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG  
AAGAGGAGAAGCTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCT  
GAGAAGAAAGCAGCGGTCCGGGCGCCACGGAGGGGCCCTCTGGGGGGACGGAAAAAAAAGAA  
GGCGCCGTCAGCCTCCGACTCCGACTCCAAGGCCGATTTCGGACGGGGCCAAGCCTGAGCCGG  
TGGCCATGGCGCGGTTCGGCGTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCGACTCCGATGTG  
TCTGTGAAGAAGCCTCCGAGGGGCGAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG  
GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG  
TGGACCGCATCAGTGAGTGGAAGCGGCGGGACGAGGCGCGGAGGCGCGAGCTGGAGGCCCGG  
CGGCGGCGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA  
GCGGAGGCGCGAGCGGGCCGACCGCGGGGAGGCTGAGCGGGGCGAGCGGCGGCAGCAGCGGGG  
ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGGT  
CCCCCGTCTCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAAGAAATCAGC  
GAAGAAGCCGCAGTCTCAAGCACAGAGCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG  
TGCGGCCCCGAGGAGAAGCAACAAGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC  
GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAAGAGCCCTCCGTGGAGGAGAAGCT  
GCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAAGGTCGACAGCCCGGACGTGAAGAGGT  
GCCTGAATGCCCTAGAGGAGCTGGGAACCTGCAGGTGACCTCTCAGATCCTCCAGAAGAAC  
ACAGACGTGGTGGCCACCTTGAAGAAGATTTCGCCGTTACAAAGCGAACAAGGACGTAATGGA  
GAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGCGGGTCTTCGGCCCCAAGATCGAGGCGG  
TGCAGAAAGTGAACAAGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG  
GAGCTGGCCGGGGAGGAGGCCCCCCCAGGAGAAGGCGGAGGACAAAGCCAGCACCAGTCTCTC  
AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGGAGGCGCAGAGGACAAGGAGCAG  
AGGAGGGTTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAG  
GTACGGGAGGGTCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCGAGAGGGCACG  
GGGGGACTCGGAGGCCCTGGACGAGGAGAGCT**TGAG**CCGCGGGGACGCCAGGCCCAGCCCCGCG  
CCGAGCTCAGGCTGCCCCCTCTCCTTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAAGTGTGGG  
GAACGCTGTGCTGTTTGTATTTGTTCCCTTGGGTTTTTTTTTCTCCTGCCTAATTTCTGTGATT  
TCCAACCAACATGAAATGACTATAAACGGTTTTTTTAATGA

amino acids 1-13

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## FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA  
ACACCATTTGAAAGAGAACATTGTTTTTCATCCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAAGA  
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTTCTCCAGTCACTGGCACTTTGAAGCA  
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCCTTTTTGGGTTCATC  
AGAAGGACTGGATTTTCAAACCTCTTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT  
CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA  
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA  
AACTCACATATATGTGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA  
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCCTCAGCAGCC  
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTTCCTTGGCAAAGATACTGCATT  
CACTCGATCCCTTGGGCCTACTCATGACCACCCTACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG  
AGCAAAATTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTTCG  
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT  
AGGAGGACAACGCAGCCTGATAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG  
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT  
AGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT  
CAGAGCAGTTTTTAATGGTCCATATGCTCATAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT  
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA  
TGATGTCATCAGTTTCATAAAGCGGCCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT  
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAGAAGATGGCCAGTACGA  
TGTAATGTTTTCTTGAACAGACATTGGAACCTGTCTCTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGGAAATATGGA  
AGAGGTAGTGTGAGGAGGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA  
GCAACAATTGTACATTGGTTCCCGAGATGGATTAGTTCAGCTCTCCTTGCACAGATGCGACACTTATGGGAAAGC  
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCCTGGGATGGAAATGCATGCTCTCGATATGCTCCTAC  
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCACCCAGTGCTGGGACATCGAAGACAG  
CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC  
TAAATCCCAACAAGCAACTATTAATGGTATATCCAGAGGTGAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA  
TGAAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG  
CAAAGCCCAGGAGCACACTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA  
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA  
CTACATCCAAATCCTTAGCAGCCCAAACCTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG  
GAGACAGAGAAACAAGGGGGGCCAAAGTGGGAAGCACATGCAGGAATGAAGAAGAAACGAAATCGAAGACATCA  
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCAGTAGTTTCTTACTTAATTTAAAGAAAAGAATTCCTTACC  
TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTTGCTAAGG  
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCATTTGAACCAGTTTT  
CCAAGAACAATCTTGACAAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA  
TGTTTTGAGTTTTTGAATTTATTGTTCATGTAAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGATAAGGT  
GCTTTATTTCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT  
CATTCTATTGAGAACCAGCTACCTTGTGGTAGGGAAATAAGAGGTGAGACACAAATTAAGACAACCTCCATTATC  
AACAGGAACCTTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC  
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT  
ATTGACTAGTCAGGAGTAACAGGTTTCACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA  
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTTAATAAAAACAAGGAAAACA  
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT  
AAATTCTGGCTTTGGGGAAAACCTCATATCCCCATGAAAAGGAAGAACAATCACAAATAAAGTGAGAGTAATGTAA  
TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAATCTAGATTATAACA  
AACTGCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC  
AATGATATTTTCAGTATATATTTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTACTGC  
CTTTATTCTCTCTGTATATTGGATTTTGTGATTATATTTGAGTGAATAGGAGAAAAACAATATATAACACACAGA  
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTTGTTGAATAACAGAACGAGTGTAAAATTTTAAC  
AACGGAAAGGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT  
GTAGTATTGTTTTTGTAAATTTAACAATAAATAAGCCTGCTACATGT

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## **FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFL  
 GSSEGLDFQTLLLDEERGRLLLGA KDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA  
 NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD  
 PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLN GAKFIGTFF  
 IPDTYNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC  
 SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP  
 YAHKESADHRWVQYDGRIPIYPRPGTCPSKTYDPLIKSTRDFPDVISFIKRHSVMYKSVYPV  
 AGGPTEFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEE  
 LQIFKHSSIIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNA  
 CSRYAPTSKRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECIPKSQQA  
 TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMY YCKAQEHTFIHTIVKLT LN  
 VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN  
 KGGPKWKHMQEMKKKRNRHRDLDELPRAVAT

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-36

#### **N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

#### **Tyrosine kinase phosphorylation site.**

amino acids 571-576

#### **Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

## FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTCATCCTGGAGCATGCCACCGCGGGGAGCAGA  
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC  
CTCAGCAGTTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGAGCAGAAGGCGTGGCTGGCAAGA  
GTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATGGGCATC  
GGGTGAGGTGGGGGGGCACAGGTGTCTGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG  
AGCCATTGAGGGTGTCTATGGAGCTACAGAGGGGAGGAAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA  
GAGCACAGTTTTTTGGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTGTGCTTCCTAGTTCTGTAGCCCCAGGT  
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCATCTAAAGTAGGGCCAATAATAGCACCCACCTCAT  
AGGGAAGATTAAATGACATAATGTATGTGATGCACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG  
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT  
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCCGGGCACAGGTGAGCC  
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGGCGGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC  
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCCC  
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCCGACACGCTGGTATTTGCTATCAGGCAGGGCGTGAGGATG  
AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTCTAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCAGAGAGCAGCC  
AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCTCTGGCACAGGCCCTGTACAGCTACACCGGACAGA  
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCCGGGCCCAAGATGGAGTAGATGACG  
GCTTCTGGAGGGGAGAATTTGGGGGCCGTGTGGGGTCTTCCCTCCCTGCTGGTGGAAGAGCTGCTTGGCCCCC  
CAGGGCCACCTGAACTCTCTGACCCTGAACAGATGCTGCCGTCCCTTCTCCTCCAGCTTCTCCCCACCTGCAC  
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGACAAAGCCCTGGACTTCCCTGGGTTCTCTGG  
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCGGCTAAAGCCCCGGATCCTGGCCACC  
CAGATCCCCTCACCTGAAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGCTGTCCCTATCTTCAAGCTGTGAGA  
CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCTCACCTCCAAGGGT  
GGAACTTGCCCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTTCCATTGTTCTATCATCTCTAGGACC  
GGAATACTACTACCTTCTCTTCTGTCTATGACCTATCTAGGGTGGTGAATGCCTGAAATCTCTGGGGCTGGAAACC  
ATCCATCAAGGTCTCTAGTAGTTCTGGCCCACTCTTCCCCACCTTGGCTCCATGACCCACCCCACTCTGGATG  
CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG  
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCCTCTTGTG  
CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACCACGGGCAGGGGCTGCTCCAGCTGCCAC  
GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC  
TGAGGGGTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC  
AGCTGGGGGGCAGTGCTGTCCAGTGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG  
TCCATCAGCACAATGAAGGAGACTTGAGAGAAGAGGAAGAATAACACTGTTGCTTCCCTGTTCAAGCTGTGTCCAGC  
TTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAAAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC  
AGTTTACTCTGGGGGTTTCAGGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA  
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGG  
TCAACAATGAGAGACCAGGAGTAGGTCCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCCAGCCAGTGTC  
AGTCCCGGCTGTGTTTTCTACCTGGTGATCAGAAGTGCTGGTTTGTCTGGCTGCCCATTTGCCTCTTGAGTGG  
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTG  
CACGAGGGGTTAGGCTGCTGTCCCTGAGTCCCTCCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC  
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCAGACCCCTGACCACCCCTG  
GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT  
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG  
GCCCTCCCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTC  
AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCCAAGGCCACTT  
TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCCA  
CAGAGAACACAGTGGTCTCCCTGTCCGGGGCGGCTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGAGGAG  
GCCTCTTGTGCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC  
CGTCTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT  
TCATGTTTTGTTTCTTACGTTCTTTCAGCATGCTCCTTAAAACCCAGAAAGCCCCAATTTCCCCAAGCCCCATTT  
TTTCTTGTCTTTATCTAATAAACTCAATATTAAG

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## **FIGURE 178**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA  
QVSQVKGAAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS  
DFEECEETGELFEEPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEW  
VKARNQHGEVGVFPERYLNFPDLSLPESQSDNPGCAEPTAFLAQALYSYTGQSAEELSFP  
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPPELSDPEQMLPSPSPPS  
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT



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## FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA  
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGAGTCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA  
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG  
GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTTCTTTAACGGTCTCAGCCCTTCTGAAAACCTTTGCC  
TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT  
GCCCTAGACGGCCTCAGTCCCTCCCAGCTGCAGTACCAGTATGCTCCAGTCCAGACAGGCTCGCATCCCGGAGGGG  
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCCTGCCTCCTGCCATTTGTGCCGCTCTCCTGGCTGGTGTG  
GCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGGAGAT  
CGTGTTCAGAGAAGCTCAACGGCAGCGTCTGCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTGCA  
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGACAGTGCAGTA  
CCTGGGCCAGGCGCCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC  
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGGAGCCCTGTTAGGCGTGTACAATATCGGGGGGCTGAACTCCA  
CCTCCAGCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCTACGCCGGAAGAGTCC  
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAGCCCCAGCCCCAGACCCCGAAGAGCCAA  
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGTGC  
GGGGCTAAAGCGCTACCTGCTAACAGTGTGGCAGCAGCAGCCAAAGGCCTTCAAGCACCCAAGCATCCGCAATCC  
TGTGAGCTTGGTGGTGAATCGGCTAGTGATCTGGGGTCAGGCGAGGAGGGGGCCCCAAGTGGGGGGCTGAACTCC  
CCAGACCCTGCGCAGCTTCTGTGCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGGCTGACCACTTTGA  
CACAGCCATTCTGTTTACCCGTCAGGACCTGTGTGGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGGG  
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA  
TGAATGGGTGATGCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTTGAATGGGCCTTTGAGCAC  
CTCTCGCATGTGATGGCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCTGTCAGTGGCCGCTT  
CATCACTGACTTCTGGACAATGGCTATGGGCATGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT  
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGGCCGACTCACGCCATTGTCC  
ACAGCTGCCGCGCCCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAACA  
CTCGCCCTGGGCGGATGGCACACCCCTGCGGGCCCCGCACAGGCTGCATGGGTGGTGGCTGCCCTCCACATGGACCA  
GCTCCAGGACTTCAATATTTCCACAGGCTGGTGGCTGGGGTCTTGGGGACCATGGGGTGAATGCTCTCGGACCTG  
TGGGGGTGGTGTCCAGTTCTCCTCCCGAGACTGCACAGGCTGTCTCCCGGAATGGTGGCAAGTACTGTGAGGG  
CCGCGGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA  
GTGTGCTGCCTACAACCACCGCACCGACCTCTCAAGAGCTTCCCAGGGCCATGGACTGGGTTCTCGCTACAC  
AGGCGTGGCCCCCAGGACCAGTGCAAACTCACCTGCCAGGCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC  
ACGGGTGGTAGATGGGACCCCTGTTCCTCCCGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG  
CTGTGATCGCATATTGGCTCCAAGAAGAAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTTCTGGTTGCAG  
CAAGCAGTCAGGCTCCTTCAGGAAATTAGGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGGCCACCCA  
CATTCTTGTCCGGCAGCAGGGAAACCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA  
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGCTTGCCTA  
CAGCGGGGCCACTGCAGCCTCAGAGACACTGTGAGCCATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCCCT  
AGTGGCTGGCAACCCCCAGGACACACGCTCCGATACAGCTTCTTCGTGCCCGGGCCGACCCCTTCAACGCCACG  
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCCCTGGGCGGGCAG  
GAAATAACTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT  
CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCTGAGACCTGCCCTCCTCTCTGCCCTAAT  
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGGCACTGATGGGTAGTGGATGGAAGGGGCTGACAGAC  
AGCCCTCCATCTAAACTGCCCTCTGCCCTGCGGGTCAAGGAGGGAGGGGGAAGGAGGGAGGGCTGGGCC  
CAGTTGTATTTATTTAGTATTTATTTACTTTTATTTAGCACAGGGGAAGGGGACAAGGACTAGGGTCTGGGGAA  
CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGTG  
TGTGTATGCGTGTGTGTGTGTGTGAAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTTCTC  
TTCCTGAATTTTATTTTGGGAAAAGAAAAGTCAAGGGTAGGGTGGGCCTCAGGGAGTGAGGGATTATCTTTT  
TTTTTTTTTCTTTCTTTCTTTTCTTTTCTTTTGGAGACAGAATCTCGCTCTGTGCCCCAGGCTGGAGTGCAATG  
GCACAATCTCGGCTCACTGCATCCTCCGCTCCCGGGTCAAGTGATTCTCATGCCTCAGCCCTCCTGAGTAGCTG  
GGATTACAGGCTCCTGCCACCACGCCCAGCTAATTTTGTGTTTGTGTTTGGAGACAGAGTCTCGCTATTGTC  
ACCAGGGCTGGAATGATTTCACTCACTGCAACCTTCGCCACCTGGGTTCAGCAATTCTCCTGCCTCAGCCTCC  
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCCGCTAATTTTGTATTTTGTAGTAGAGACGGGGTTTAC  
CATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTTAGGTGATCCACTCGCCTTCATCTCCCAAAGTGTGGGATT  
ACAGGCGTGAGCCACCGTGCCTGGCCACGCCCCAATAATTTTGTATTTTGTAGTAGAGACAGGGTTTACCATGT  
TGGCCAGGCTGCTCTTGAATCCTGACCTCAGGTAATCGACCTGCCTCGGCCCTCCCAAAGTGTGGGATTACAGG  
TGTGAGCCACCACGCCCCGTACATATTTTAAATTGAATTCTACTATTTATGTATCCTTTTGGAGTCAGACAG



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## FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV  
FPEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP  
GTYLTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP  
ASGQGPMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA  
AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF  
DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD  
NSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL  
PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG  
PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRVPVRNGGKY  
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK  
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG  
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL  
MPSPTDVVLPGAVSLRYSYGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT  
PSTPRPTPDWLHRRRAQILEILRRRPWAGRK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-  
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-  
582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 358-367

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## FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCA**ATGG**  
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC  
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT  
AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG  
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA  
TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
ACAACCTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
CCTGCCAACGAAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG  
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT  
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
CTGCTACCAAGGAGGACGAGTCATCTGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC  
GCATGCTGGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT  
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT  
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
AAAAAAAAAAAAAAAAAAAA

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## **FIGURE 182**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLEDERGYCCIIYCRGRNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-40

#### **Transmembrane domain:**

amino acids 25-47 (type II)

#### **N-glycosylation sites.**

amino acids 94-97, 180-183

#### **Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

#### **N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

#### **Microbodies C-terminal targeting signal.**

amino acids 315-317

#### **Cytochrome c family heme-binding site signature.**

amino acids 9-14

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# **FIGURE 183**

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC  
 CCGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG  
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
 CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
 GCGCCTGCGCCGTCAATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
 ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA  
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTTGGT  
 GGCACCCTGCTTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC  
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
**TGAG**TCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA  
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA  
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT  
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

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## **FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTTPAKTTFAILGGTL  
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ  
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

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## FIGURE 185

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCTCT  
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC  
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
GTGAGGCAGAGTTTCAAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC  
CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC  
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
AACATGACACTGACCTCCGGGATCATGTTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT  
GTCTGTGTTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG  
GCATGGGTGGGATGGTGCAGACTGTTTACAGACCAGGTACACATTTGGTGCGGCTCTGTTTCGTG  
GGCTGGGTGCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCTGCCGGGG  
CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTG  
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG  
ATATACGATGGAGGTGCCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  
TGT**GTAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA  
AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC  
CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC  
ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT  
TTCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC  
ATTTTGATGATTTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTA  
TTTCCCAGCTTATCCCCAAGAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT  
CTGCTGTTTGAATTTTGTCTCCCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA  
GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
TGATCTTAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG  
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG  
TCCTCTTTCTGTGCGGGTCCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT  
TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGA  
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT  
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC  
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG  
GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG  
GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG  
AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA  
ACTAATTCTTTAA



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## **FIGURE 186**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRQSSGFTE  
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM  
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL  
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE  
DEVQSYPSKHDYV

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

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## FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG  
GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATA**ATG**GCAACCCATGCCTTAGAAATCGCTG  
GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG  
AGAGTGTCGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTTCTGGGAAGGACTGTG  
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG  
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC  
TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA  
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT  
GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGGCACTGGTGTCT  
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTGTGCAACGAAAAGAGCAGTAGCTACA  
GATACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG  
AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTGTATGTTTTTTTAACTTTACTATAAAGC  
CATGCAAATGACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTA  
CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA  
GCTATTTTCAGCAGAATGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT  
TTGTTTTCTAAGGTGGTTC AAGCATCTACTCTTTTTATCATTTACTTCAAAATGACATTGCT  
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG  
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG  
AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGA  
AGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTG  
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTT  
TTCTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA  
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
GTTTTAGGAAAGTGAAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA  
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACA  
ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG  
TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTACCATTTCTGTTTAGTTTTACTAAA  
ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGA  
AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA  
TTAATAAATTGTACATTTTTTCTAATT

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## **FIGURE 188**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM  
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI  
IFIITGMVVLIPVSWVANAIIRDFFYNIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF  
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## FIGURE 189

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTTCGGCTTGCTGGTCTACCTTGCTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA  
TTGTCTTTGTTCATCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGTTGCTGTGCTGCACTT  
GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCCT  
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTTGACGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT  
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTTCTTTTGAAGTATTTTAAATTCATTT  
GAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC  
CAGTCAAGCTATGGAACATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG  
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCACCTCCGGAACCTTCTGACCTCTGTTTCCTCCGTCCTGATAAGACG  
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTTACACTCACATTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA

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## **FIGURE 190**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM  
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV  
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGLGWAASGLLLLGGGLLCCTCP  
SGGSQGPPSHYMARYSTSAPAISRGPPSEYPTKNYV

### **Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

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## FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG  
 AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC  
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTTCCTTGGCATGGTGGGGACTCTTGCCACAACCCT  
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGTTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
 TGGGAAGGGCTCTGGATGAAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
 TAGCTCCTTGTTGGCTCTCCCGCCTGCCCTGGAAACAGCCCCGGGCCCTCATGTGTGTGGCTG  
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
 GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCCTCTTCATCCTGAC  
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
 ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA  
 AGCGCTGCTGTCCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA  
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT  
 ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA  
 GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG  
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
 GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG  
 TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
 GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

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## **FIGURE 192**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER

AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL

FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

### **Important features of the protein:**

#### **Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

#### **N-glycosylation site.**

amino acids 161-164

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## **FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATGA**AAGATCACTGGGGGT  
 CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
 AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
 CATACTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC  
 GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA  
 TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
 AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG  
 ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
 TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCCAGA



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## **FIGURE 194**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN  
ECHLCTESLKSNQGRVQFLHDGSC

**Signal peptide:**

amino acids 1-19

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## FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCC**ATG**GCTGCCTCCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTAC**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTC  
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT  
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT  
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

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## **FIGURE 196**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFL  
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRDRNGHEYYGDYYQRHYD  
EDSAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

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## **FIGURE 197**

CGGCTCGAGCCCGCCCGGAAGTGCCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC  
GGTAGCGCGGGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC  
CGTCCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCCTGGGTCTCAACGCACA  
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCCAGC  
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT  
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGGTTACAGCAACACCGCCAG  
CCCCGGACTCCCCGCAGGAGCCCCTCGTGCTACGGCTGAAATTCCTCAATGATTCAGAGCAG  
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG  
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG  
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC  
CCAAATCCCCCTGCCCGCCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT  
GCTGCTGCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
CCTTCTTTCCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCACCCTGCTCCTCAGTCTCCTG  
GCCTTTGCCATGTACCGCCCC**TAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC  
GGACCTTGCTCCCCGCGCCGCGGGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG  
CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGCAGAGGACTCCCGGGACTGGCGGAGG  
CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA  
CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTGCTGCCTCGGCCCCGGGCAGAGCCG  
GGCCGCCCCGGGGGCCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCTCCAATCCCTGAC  
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG  
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTAAAAA  
AAAAA

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## **FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRRLKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVSTRVGPPNPPCPPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

GAGATTGGAAACAGGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG  
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCTAAGAACCATCAGCCC  
TCAGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGC  
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT  
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG  
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC  
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA  
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGCATCCACTGCGCAAAAAGGA  
TTGTGTCCGGAGCACGGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTCAGGCCGG  
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATTGAAACAGGGTGCGGGTGACCCGTGG  
AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTTCATTTCTTCTTCTTCTACTGCCTCCA  
CTTCATGTTATTTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAA  
TGGTTTTTCTTGGCTTCCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCCTGTCTGTTAT  
TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

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## **FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI  
NENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLLAGIHCAKRIVSGARGMN  
NWVEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

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## FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA  
CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG  
CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTC  
AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC  
TTGGGGTGAAACTTGGGTCCCTGTGGTCTTCTGATTGTAAGTGGAAGCAGGTCTTGACACGC  
TGTTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA  
ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC  
CTGTTGCATTTGGCAAGTTCTAGCAAC**ATG**CTCCTAAGGAAGCGATACAGGCACAGACCATG  
CAGACTCCAGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT  
TGCACCCCTCCCCACCACACCCTGCACCAGACTGTACAGCCCAAGCCAGCAAGCACAGCCCT  
GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA  
GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC  
TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG  
AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG  
GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACGCCTGGACCCAC  
GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG  
CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG  
TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC  
CCAGGGCCTTCTGAAGGAGATCATCCTCGTGACGACCTCAGCCAGCAAGGACAACCTCAAG  
TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG  
GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT  
TCATGGATGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCTCCTCAGCAGAATAGCT  
GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA  
TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAAC  
CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG  
GTGCCCCGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC  
TCTTATGTCGCTGCGAGGTGGTGA AACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTG  
GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT  
TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTTCGCATTGCTGAGACCTGGCTGGG  
GTCATTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA  
AGCCAGACTGCATGGAACGCTTGCACTGCAAAAGGAGACTGGGTGTGCGGACATTCCACTGG  
TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA  
GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT  
GTCCCATGGTGTGGCTCCTTGCACTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTCAGGCAGGAGCAGGT  
GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG  
AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC  
AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTTGACCA  
GATAAATGCTGTGGATGAACGAT**TGA**ATGTCAATGTCAGAAGGAAAAGAGAATTTTGGCCATC  
AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT  
GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT  
TCACACCTTATTTCAATTGACTGCTGGCTGCTTA



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## **FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFG  
 ESQDWVLEAEDEGE EYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR  
 RQDKEAPKRDWGADEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
 QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR  
 LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP  
 VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD  
 RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDQSHSPLDQEATL  
 RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPCMERLQLQRRRLGCRTFHWFLANVYPEL  
 YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP  
 QHLCFAVRQEQVILQNCTEEGLAIHQQHWDFQENGMIVHILSGKCM EAVVQENNKDLYLRPC  
 DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

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# **FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTCACAGCTGAGGAAGACCTCAGAC**ATGGA**  
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC  
 TGCCCCCTCCCACCGCCTGCTCAGGGCTCTTCATCCTCCCCTCGAACCCACACAGCCCCAGCC  
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCCCACGTCATGTGTGCGTGTGGGAGCGAGC  
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCCAAGATCACGTGCGCAAGTCCTGCCTGGCACTG  
 CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCGGCCCTCATCCCAATACCCCTGGGCT  
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG  
 ATTTCTGGACTATGGTTTTGCAGCCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCCTGCGGGCCATTC  
 CTGTTCTGGGGGCGCTGGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT  
 CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
 GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA  
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCTTCGGGGACTCACCTACCCCCACCCC  
 TGACCATGAGGAGCCCCGAGGGGGACCCCGGCCCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
 CCTTCCAGTTGAACCGG**TGA**GGGCAGGGGCAATGGGATGGGAGGGCAAAGAGGGGAAGGCAAC  
 TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC  
 CTCCCACAGCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCCTTC  
 CTTCTCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCATAACTCCAACCTTGCCCC  
 TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACTCTGCCCTCTTAACCTTGATTCCC  
 CCTCTTTGTCTTGAACCTTCCCCCTTCTATTCTGGCCTACCCCTTGTTTCTGACTGTGCCCTT  
 TCCCTCTTCTCTCAGGATTCCCCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC  
 AAGCAGGAGGCCAAGGGGCGGCACAGCCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA  
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCCTTGACACACCACCGGAACACTCCCCAGCC  
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG  
 GGTCCCTGTCCCCACCCCTTGTGCACTCACATGAAAGCCTTGCACTACTCACCTCCACCTTAC  
 AGGCCATTTGCACACGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT  
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG  
 TGGTCAGCGTTTTCTGCACACTTTACCTCTCATGTGCGTTTTCCCGGCCTGATGTTGTGGTGG  
 TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTTCCGCAGCCCCTGC  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGGCCCTCATCGGTCATGG  
 TCTCGTCCCATTCCACACCATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA  
 TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA  
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA  
 AGGGACTCCCATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTTGTCTGTCTGGCTG  
 TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCCTCCCTTCCCAGCCT  
 CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC  
 ATCGGGAGCTCTGCCTCCAAGTCTACCCTTCCCTTCCCGGACTCCCTCCTGTCCCCCTCCTTT  
 CCTCCCTCCTTCCCTTCACTCTCCTTCCCTTTTGCTTCCCTGCCCTTTCCCCCTCCTCAGGTT  
 CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCCCTCCTTCCCTTCTTCCCTGGCTCCTAGGCT  
 GTGATATATATTTTTGTATTATCTCTTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG  
 GGATGTAAGTTTCAAAATTTTCAAATAAAGCCTTTGCAAGATAA

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## **FIGURE 204**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA  
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSP  
EMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 195-217

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## **FIGURE 205**

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGG**ATGG**  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGACACCGGTCCCC  
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC  
GGCGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA  
GGGGCCGCGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAAAAA



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## FIGURE 207

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGG  
CGGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA  
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGC  
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA  
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TA**AGTAGCCC  
CCAGAGGCGCTGGGAGTGTTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG  
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT  
CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG  
ACTCGCACGTGCCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCAC  
CTGGCTGTCATCGGGTAGGGCGGGGCCGTGGGTTAGGGGCGCACCACTTCCAAGCCTGTGT  
CCCACAGGTCCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC  
TGGCACAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG  
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGA  
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG  
GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCATAGGGTCTGGTTCC  
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC  
ATGGAGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC  
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT  
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG  
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCCTCGGGAGA  
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC  
ACGAGGGTGTCTGTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT  
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
CCGACGCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT  
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC  
GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC  
CTCAGGACCCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA  
TGTGATTAAAGTCCCTGATGTTTCTC

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## **FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK  
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER  
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

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## FIGURE 209

AGCAGGAGCAGGAGAGGGACAATGGGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT  
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG  
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCC  
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA  
 TAGCATGGTGCAAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA  
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTGCGCTGGTAGACAATGAACAACCTG  
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT  
 CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTATTCAACAGCG  
 TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG  
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTTCAAACATAAGGAGTCTCAACTGCCAG  
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC  
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCTTAAGTGGAAAATTGTTGAAAGAAAATCG  
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTCTGACTTCTCCTTGGAACCTACATATGGCC  
 AAGTATCTACTTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG  
 GATCACTAGGCCTGCCAACCACACACACACGACGTGCACACACGCACGCACGCGTGCACAC  
 ACACACGCGCACACACACACACACACAGAGCTTCATTTCTGTCTTAAAATCTCGTTTTCTC  
 TTCTTCCTTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT  
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
 CCTCTATGAAAGAGAGGCATTCTTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT  
 TTGTATACTGCACATGACTTACACACAACATAGTTCTGCTCTTTTAAGGTTACCTAAGGGT  
 TGAAACTCTACCTTCTTTTATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG  
 ATGGTTTTTAAACACCTTTGTGAAATTGTCTTTTTTGCAGAAAGTTAAAGGCTGTCTCCAAGTC  
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCCC  
 TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA



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## **FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG  
FFQDLEIPAVPILHSMVQKFPGVSFGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA  
KLFQGGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPATAEVSVEHVQNF  
CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

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## FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG  
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
GACGCGGCGGCGGGCGGCGGCGACTGCAGTGGCTGGACGATGCCAGCGTCCGCCGGAGCCGGG  
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGCTGGCGGCGGCGCTTG  
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC  
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG  
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC  
TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA  
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGC  
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC  
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC  
CTCAGCAAGAAACAAAACCAAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT  
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
ACAAAGGATATGTATAAATATTTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA  
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC  
AGGTCATTTACAATTGGGAGATTTTCAGAAACATTCCTTTACCATCATTTAGAAATGGTTTG  
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG  
GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA  
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT  
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG  
AAATGTGTCATATCAATTTCTGGATTCATAATAGCAAGATTAGCAAAGGATAAATGCCGAAG  
GTCATTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT  
GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTTA

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## **FIGURE 212**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop .

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINIEN  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI  
LAVLYRRKNSKRDTYTGCTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG  
GHHSDKINKSESVVYADIRKN

### **Signal peptide:**

amino acids 1-37

### **Transmembrane domain:**

amino acids 161-183

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# **FIGURE 213**

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGA CTGCCCCGGGCTGCCGCC  
 CCGGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC  
 TCTCGGCCACGGCTGGGTCTGGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC  
 TGGCAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCCGACCCCTGAGGCG  
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC  
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC  
 TGGTCAGAAGGTTTtaggttatgctgatgttgagaaccgtgtaccatgtaaaccagagacagt  
 tatgccaattgctagcatcagcaaaagtctcaccatggttgctcttgccaaattgtgggaag  
 cagggaaactggatcttgatatccagtagcaaacattatgttcccgaaattcccagaaaaagaa  
 tatgaaggtgaaaagggtttctgtcacaacaagattactgatttcccattttaagtggaattcg  
 tcattatgaaaaggacataaaaaagggtgaaagaagagaaagcttataaagccttgaaagatga  
 tgaaagagaatgttgcattttgagcaagaaaaagaaggcaaaagtaatgaaaagaatgattttt  
 actaaattttaaacagagcaggagaatgaagccaaatgccggaattcaaaacctggcaagaa  
 aaagaatgattttgaacaaggcgaatttatatttgagagaaaagtttgaaaattcaattgaat  
 ccctaagattattttaaaaatgatcctttgttcttcaaacctggtagtcagtttttgtattca  
 acttttggctataccctactggcagccatagtagagagagcttcaggatgtaaatatTTGGA  
 ctatatgcagaaaatatccatgacttggatatgctgacgactgtgcaggaagaaaacgagc  
 cagtgattttacaatagagcaagg**TAA**atgaataccttctgctgtgtctagctatatcgcatc  
 ttaacactattttattaattaaaagtcAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC  
 cacattttgggagcttttctacatgtctgttttctcatctgtAAAGTGAAGGAAGTAAAACA  
 TGTTTATAAAGTAAAAAAA

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## **FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQ RAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRG  
 AAPAQSPAAPDPEASPLAEPPEQEQSLAPWSPQTPAPPCSR CFARAIESSRDLLHRIKDEVGA  
 PGIVVGVSVDGKEVWSEGLGYADVENRV PCKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
 IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
 EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN  
 DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDL DMLTTVQEENEPVIYNRAR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 39-60

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## FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG  
 AGGCTGGTGGGAAGAAGCCGAG**ATGG**CGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
 TCTTGCTGATGGCGGTAGCAGCGCCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT  
 GGTGCGCGAGGGGCTGGGGCGGAAGGTTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT  
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC  
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG  
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
 TGGAGTCGCACCTGTCCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
 GTGTCCGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG  
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG  
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCTCGTCCTGTTTCCTCATGATGTCAGG  
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC  
 TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTG  
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
 TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTTCAGAAACCCAAG  
 GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
 TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA



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# FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT  
GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTTCGTCGGGGGGCCCACC  
**ATG**CTGGTGA CTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGA ACT  
GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC  
AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC  
GCAAGAATTCTTGTGTCCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAA ACTCTCT  
CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC  
CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC  
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTTCGACCGCCGC  
GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTATCTTCATCTTTGTCTTCCT  
CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTCTTCATGTTGACTTT  
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCCTTCATAGCCTTTCTACTTATTGAGT  
TGGCTTGTGGATTATACTTTCCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA  
GAGCAGGCTGGTGTACTCAACTGGTTCCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTTCAGCATTTGCTCTG  
CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTCACCGTGGTAAGGCATGATGCT  
GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCCTGAGCTG**TAA**CCCCACTCCAG  
GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTCTGT  
GACTGACTTTGTGACTGTCCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA  
ATAAACACTTTTAAATGATCAAAAAAAAAAAAA



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## **FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR  
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVI PET  
EQAGVLNWFVRVPLHSLACLGLLLVLHSDRKTGTRNMFSICSAVMVMALLAVVGLFTVVRHDA  
ELRVPSPTTEEPYAPEL

### **Signal peptide:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

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## FIGURE 219

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCCGGCCCTGGAG**ATG**  
 GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA  
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA  
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTACACAAGGTATGAGCAGATT  
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAAGTCAGCAACGGTTTCTTCATCCA  
 GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC  
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGCTCGG  
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
 TGG**TAGA**AAGAGTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
 AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA  
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG  
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT  
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
 AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCTCACTGACTTTTGTAGCAATAAA  
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 220**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ  
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF  
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

**Signal peptide:**

amino acids 1-20



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## **FIGURE 222**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDL S QRYCLMAVFNVIIYLENEDSE
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 1-24

#### **N-glycosylation site.**

amino acids 86-89

#### **N-myristoylation sites.**

amino acids 20-25, 45-50

#### **Phospholipase A2 histidine active site.**

amino acids 63-70

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## **FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGCCCCAGGGGGCCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTGCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAACCTACCCGTGGGTTCGCT**AG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAAA

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## **FIGURE 224**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLL VKSVQVK  
LGDSWDVKLGALGGNTQEVTLQPGYITKVFVAFQAFLRGMV MYTSKDRYFYFGKLDGQISS  
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNL TYSANSPVGR

**Signal peptide:**

amino acids 1-22

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## FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
 GAACTGGGTGCTCATCACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT  
 TTTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAAGCTGTAAAGATGCAAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT  
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT  
 CCCAAGGGGTCCAATTTTTCTTCTGGGTGTACGCGAGCCCTGACTCACTACAGTGCAGCTG  
 ACAGGGGCTGTCATGCAACTGGCCCCTAAGCCAAAGACCTAAGGACGACCTTTGAA  
 CAATACAAAGGATGGGTTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG  
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA  
 TATCTGCTGGTTGCTTAGGTTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT  
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
 TGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA  
 TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTTGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTTCGGGGCTTGCGGAAGCTGCTGAGTTT  
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC  
 TGGAACCTTTTGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC  
 ATGATCAGACTCAAAGAAGTTTACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT  
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTATAG  
 GACAGACCATGTCTTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC  
 GAAGCTTTTCACTGGACCCAGTGTTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA  
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACA  
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTG  
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT  
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT  
 GAGAGCAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCCTGTCCG  
 TGCTCGTCATCCTGCTGGTTATCTACGTGTGATGGAAGCGGTACCCTGCGAGCATGAAGCAG  
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT  
 GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCACCAACACGGAGACCAGCGAGA  
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
**TGA**ACCATTGTGATAAAAAGAGCTCTTAAAAGCTGGGAAATAAGTGGTGCTTTATTGAACTC  
 TGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG  
 CAAGATCCTTCCTTGTCCGTTTTAGTGCATTCATAATACTGGTCATTTTCTCTCATACATA  
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAAGTCCGGTTAATATAA  
 TACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCGATTTGTTTTAAGATAAACT  
 TCTTTCATAGGTAAAAA



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## **FIGURE 226**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301

><subunit 1 of 1, 513 aa, 1 stop

><MW: 58266, pI: 9.84, NX(S/T): 4

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG  
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF  
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELL  
DLGYNRIRSLARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTM  
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFIGQEILDSWISLNDISLA  
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKE LQGVNVIDAVKNYSICGKSTTERFDLA  
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI  
LLVIYVSWKRY PASKMKQLQQRSLMRRHRKKKRQSLKQMPSTQEFYVDYKPTNTETSEM LLN  
GTGPCTYNKSGSRECEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 420-442

#### **N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

#### **Tyrosine kinase phosphorylation site.**

amino acids 136-142

#### **N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

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## FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT  
TAAAT**ATG**TCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG  
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTTG  
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGG  
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
AAAACAACCT**TGA**TTTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA  
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA  
GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG  
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC  
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTTTCTCTGGAGCCTCAGGGCTTG  
GCATTTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT  
AAACATCAATAGATATCTAAAAA

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## **FIGURE 228**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVA

ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP

VPAPCFGPLGSPPPYEEIVKTT

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 52-70

## FIGURE 229

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA  
 GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC  
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAACT  
 CCTCTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG  
 ATGAAGAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGC  
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTTGCTTCTTCAGAAATGTTTTTTA  
 CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATT  
 TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAATACTAGACTTAAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT  
 GCTGTCTTCTGGATGACATTTTGAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT  
 TGTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA  
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTTCATGGAAC  
 TCTAATTCTGTACATAAAAAATTTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG  
 CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTC  
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGGACAAGTGAAGAATGTTTAA  
 TCATTCTGTCATTTGTTCTCAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAAATGTG  
 CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTGCACTATCCTTCAGAATAACTGA  
 AGGTAAATTATTGTATATTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTAATAACAGCATTAAAATAGTT  
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTTATGATGAGAGTAACAATA  
 AAGTATTCATGATTTTTTACATACATGAATGTTTCAATTTAAAAGTTTAATCCTTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTAAATTTTGCTTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTTAGCCAGGTGTATATAATAAA  
 GGTACTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTTAACATTATATTATATAAGAGTATC  
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC  
 TTAAAATAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT  
 GTATATAGCACAGGGAACCTAATCTTGGGTAATTCTAGTATAAAACAAATTATACTTTTAT  
 TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT  
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT  
 TGTATTGTTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAATA  
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTTCTCTCTCTCTGTA  
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

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## **FIGURE 230**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE  
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL  
VPVTTNKRTNVSGSIR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

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## FIGURE 231

CGCGGCCGGGGCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
**CATG**CCGTGGCCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCCAGACAACCCGGCCATGCT  
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG  
 GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA  
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTTGGCGGGGCCGGGCT  
 ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCTGCTGCC  
 TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
 AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG  
 AGGTCTCAGTGCTCGCCTTCACGACGCACAGTCAGGGCCGGGCACTACAGCTGGACCTCTCC  
 CACAACCTCATTCACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCACCAT  
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC  
 TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCATTGGTCCGGGTGCCTTCGCGGGG  
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
 TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCTTGACCTGTCGGGCAACCCCAAGCTTAACCT  
 GGGCAGGAGCTGAGGTGTTTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC  
 AACCTGGTGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT  
 GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCGGAGGCCTGGCT  
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC  
 ATCTTGT**GACA**CAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTCTGGGCTGCCTCAG  
 GTCCCGAGTAACCTTATGTTCAATGTGCCAACACAGTGAGGGAGCCCGCAGGCCTATGTGGCA  
 GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
 AAAGTCTCACCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA  
 AACCAGACTCGGGTCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCCTTCCCTCAT  
 GCCTGGGGCCGGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
 GTTCAGGTCCACTGGGCTGAGTGTCCTTGGGCCCAGTGGCCAGTCACTCAGGGGCGAGTT  
 TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT  
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCTTCTCATGTGAC  
 AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC  
 ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCCGGACCCAATGCACTTTCTTGTCTCCTCTA  
 ATAAGCCCCACCCTCCCCGCCTGGGCTCCCCTTGCTGCCCTTGCTGTTCCTTATGACACA  
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT  
 GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT  
 CCAGCCTAGCCAGTTTCTCACCCTGGGTGGGGTCCCCCAGCATCCAGACTGGAAACCTACC  
 CATTTTCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA  
 TCTGGCTGGGATCTCCAAGGGGCCTCCTGGATTGAGTCCCCACTGGCCCTGAGCACGACAGC  
 CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGTCTATGC  
 TCTACCCCCAGGGCAGCATCTCAGCTTCGAACCTGGGCTGTTTCCTTAGTCTTCATTTTA  
 TAAAAGTTGTTGCCTTTTTTAACGGAGTGTCACCTTCAACCGGCCTCCCCTACCCCTGCTGGC  
 CGGGGATGGAGACATGTCATTTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAAT  
 ATTGTCTGGGCCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCCACCTGCCTAGC  
 CCATCATCTATCTAACCGGTCCTTGATTTAATAAACACTATAAAAGGTTTAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop .

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLLAVSGAQTTTRPCFPGCQCEVETFGFLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH  
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP  
AESFTSSPLSDVNLSHNQLREVSVSFAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI  
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGGLTHLSLASLQRLPELAPS  
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV  
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

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## FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG  
GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA  
AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC  
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCC  
TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA  
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC  
GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
GCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC  
TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTTCGAGGT  
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT  
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT  
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTTGTAAATATCTT  
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTT  
ATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
AGCAGGTGATGTATTTTTTATACAGTAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT  
AGGGGGGTATTCAATTTGTATTCACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT  
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT  
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA  
CCAAAAAAAAAAAAAAAAAAAA



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## **FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

><subunit 1 of 1, 261 aa, 1 stop

><MW: 29667, pI: 8.76, NX(S/T): 0

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP  
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL  
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP  
DHYTLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG  
ELDILLQWMEETE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

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## **FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA  
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVKSEDEH  
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFKILAEGLI  
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNLTPLEDNIMTHGLSSSLCSGLVASILGTP  
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT  
YEKIREMSGVSPF

### **Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

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## FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC  
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCTCGCAGGTATATTGTTTTTTACAGGC  
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
TCACACATGTGGTGTATTTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC  
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTTGGTGC  
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTTCAAATGCACTTA  
TATTTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC  
TTCTTAAGTCACATTTTCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT  
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTTATGTTT  
TGAGTTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA  
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTTATTCCTGAGATTTAGAA  
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT  
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG  
CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT  
AAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC  
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
TAAAGGTTTTTCAGCAAGTTGTAACCTTATTTTGGCCTAAAAATGAGGTTTTTTTTGGTAAAGA  
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC  
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA

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## **FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAAVVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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## FIGURE 239

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
 CTGGCGGCCCCGCAACACTCCGTCTCACCCCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCT  
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT  
 GGTCAGCTGGGTCAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG  
**GATG**AGAGTGTGTCAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
 TGTTTATTTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
 GCCTCGCCCAACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC  
 AGCCAACTACTTTGCGTTTAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC  
 GCCCTGGTGAATGGAACACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGGTGCACTGGTGCTGGTGG  
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG  
 GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
 CCTCAGGGGTAAAAGCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACG  
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTT**TAG**GGTGGC  
 TGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG  
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGCTGCGTGGAAGGTGCTGCAGGTCCTTGCACGC  
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCCTCCCACAGCACATCCTACCCGGAAGACC  
 AGCCTCAGAGGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGG  
 ACTGCTGACGGCTGGTCCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA  
 TTTTGTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP  
 ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
 DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD  
 LRKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:**

**Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

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## FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT  
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA  
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC  
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCCTCTAGTCCTCAAATCCCAGTCCC  
 CTGCACCCCTTCTGGGACACT**ATG**TTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC  
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA  
 GCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGT  
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC  
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG  
 GGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC  
 CCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC  
 ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT  
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG  
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT  
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT  
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA  
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTTCATCCAAGCAGGA  
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG  
 CCTTCTCCTGGCTGTTTTATTTCATTGCTAGAAAGATTCCGAAGAAGAGGCTGGAAAACCGAA  
 AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCA**TAA**ATTCCTTCTCAGATACCA  
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG  
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAG  
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA  
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGG  
 GAAGTTTGGGATATACCCCAAAGTCCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA  
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA  
 TATTTGGAAATTAAAGTTTCTGACTTT



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## **FIGURE 242**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812

><subunit 1 of 1, 337 aa, 1 stop

><MW: 37668, pI: 6.27, NX(S/T): 1

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPA SYPECGNNAQSPIDIQTDSVTFDPDLP  
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQ  
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH  
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT  
L FSTEEEPSKLLVQNYRALQPLNQRMVFASF IQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF  
IARKIRKKRLENRKSVVFTSAQATTEA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-15

#### **Transmembrane domain:**

amino acids 291-310

#### **N-glycosylation site.**

amino acids 213-216

#### **Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69



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## **FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDLHLLNPAAGMTPGTQTHPLTLGGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

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## FIGURE 245

GGAGAGAGGGCGCGGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG  
GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCG  
GCAGCCGGGAGCC**ATG**CGACCCCAGGGCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCC  
TGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG  
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG  
GCCAGCAGGAGTGCCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG  
GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG  
GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT  
TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTTCACATTC  
AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG  
CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTTCAGATTACCCAAA  
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TA**  
**A**ATGCTTTAATTTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT  
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA  
CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGT  
GGTTTCAATATTTTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA  
TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT  
AAAAATTATTTCCAACA

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## **FIGURE 246**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA  
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAEC SGPLPIEAI IYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDY PKGDASTGWNSVSR III EELPK

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 195-217